













XX DE Methanococcus jannaschii circular chromosome.  
XX XX  
XX KW Methanococcus jannaschii; methanogenic archaeon; circular chromosome;  
KW genome; autotrophic; extrachromosomal element; identification; ds.  
XX OS  
XX XX Methanococcus jannaschii.  
XX XX  
XX PN W0907840-A2.  
XX XX  
XX PP 26 FEB-1998.  
XX XX  
XX PF 22-AUG-1997; 97W0-0514900.  
XX XX  
XX PR 22-AUG-1996; 960S-0024428.  
XX XX  
XX PA (GENO ) INST GENOMIC RES.  
XX PA (UNIT ) UNIV ILLINOIS FOUND.  
XX PA (OYJO ) UNIV JOHNS HOPKINS SCHOL MEDICINE.  
XX XX  
XX PF Bull CJL Smith BO, Venter JC, White GR, Woese CR;  
XX XX  
XX XX WPT: 1998-169145/15.  
XX XX  
XX XX Complete genome sequence of methanogenic archaeon, Methanococcus  
XX PF jannaschii, useful in identification of M. jannaschii genome  
XX PF fragment  
XX XX  
XX PR claim 13; Page 152-585; 614pp; English.  
XX XX  
XX CC The present sequence represents the complete 1.66-megabase pair genome  
XX CC sequence of the Methanococcus jannaschii circular chromosome. The  
XX CC present invention describes M. jannaschii open reading frames from the  
XX CC genome sequence, the invention also describes a computer based system  
XX CC for identifying fragments of the M. jannaschii genome that are  
XX CC homologous to target nucleotide sequences, comprising: (a) data storage  
XX CC means comprising the nucleotide sequence of the 1664976, 58407 or 16550  
XX CC bp sequence (see V21209, V21210 and V21211), or a nucleotide sequence at  
XX CC least 95.9% identical to it; (b) search means for comparing a target  
XX CC sequence to the nucleotide sequence of the data storage means to  
XX CC identify a homologous sequence, and (c) retrieval means for obtaining  
XX CC the homologous sequence. The method, which is based on whole genome  
XX CC random sequencing of an autotrophic archaeon M. jannaschii, the genome  
XX CC of which consists of 3 physically distinct elements, a large circular  
XX CC chromosome (the 1664976 bp sequence given in V21209), a large circular  
XX CC extra-chromosomal element (the 58407 bp sequence given in V21210), and a  
XX CC small circular extra chromosomal element (the 16550 bp sequence given in  
XX CC V21211), can be used in the identification of M. jannaschii genome  
XX CC fragment.  
XX XX  
XX PR Sequence 1664976 bp; 568133 A; 264649 C; 258701 G; 574392 T; 101 other;  
XX XX  
XX XX Query Match 12.6%; Score 42.8; DB 19; Length 1664976;  
XX XX Best Local Similarity 64.5%; Prev. No. 11;  
XX XX Matches 49; Conserved Pct 0; Mismatches 27; Indels 0; Gaps 0;  
XX XX  
XX QY 4 aaagaqaatcaatgaatcttttcaatcttttttaataaagaatgaatattatgaat 64  
XX XX 111 111111 11111 1111111 111 111 111 111 111 111 111  
XX DB #5183 aqaatataatcaatgaatcttttcaatcttttttaataaagaatgaatattatgaat 85242  
XX XX  
XX QY 64 qatataatgaatcttt 79  
XX XX 111 111 1111  
XX DB #5243 tttaaaatcattata 85258  
XX XX  
XX RESULT 10  
XX X61446/c  
XX Db X61446 standard; cDNA; 1049 bp.  
XX A\* X61446;  
XX XX  
XX DT 14-JUL-1999 (first entry)

XX XX  
XX DE RNA encoding a human secreted protein.  
XX XX  
XX KW Human secreted protein; cancer; tumor; neurodegenerative disorder;  
KW developmental abnormality; fetal deficiency; blood disorder; leukemia;  
KW immune system disease; autoimmune disease; hepatic disease;  
KW renal disease; lymphoma; inflammation; allergy; ischemic shock;  
KW Alzheimer's; connective disorder; schizophrania; prostate disease;  
KW density; osteoclast; osteoporosis; arthritis; malnutrition; breast disease;  
KW lung disease; thymus disease; digestive disorder; endocrine disorder;  
XX XX  
XX OS  
XX XX Homo sapiens.  
XX XX  
XX PN W09922243-A1.  
XX XX  
XX PP 06 MAY 1999.  
XX XX  
XX PF 23-OCT-1998; 96W0-0522476.  
XX XX  
XX PR 24-OCT-1997; 970S-0064387.  
XX PR 24-OCT-1997; 970S-0062704.  
XX PR 24-OCT-1997; 970S-0064088.  
XX PR 24-OCT-1997; 970S-0064089.  
XX PR 24-OCT-1997; 970S-0064090.  
XX PR 24-OCT-1997; 970S-0064091.  
XX PR 24-OCT-1997; 970S-0064092.  
XX PR 24-OCT-1997; 970S-0064097.  
XX PR 24-OCT-1997; 970S-0064098.  
XX PR 24-OCT-1997; 970S-0064099.  
XX PR 24-OCT-1997; 970S-0064100.  
XX PR 24-OCT-1997; 970S-0064101.  
XX PR 24-OCT-1997; 970S-0064109.  
XX PR 24-OCT-1997; 970S-0064110.  
XX PR 24-OCT-1997; 970S-0064111.  
XX PR 24-OCT-1997; 970S-0064148.  
XX PR 24-OCT-1997; 970S-0064386.  
XX XX  
XX XX (HOMA ) HUMAN GENOME SCI INC.  
XX XX  
XX PF Brown LA, Carter KC, Iann DR, Elmer PC, Endress GA;  
XX PF Peng P, Florence C, Florence KA, Greene JM, Janat P;  
XX PF Kaye W, Lathier DW, Moore PA, Nijl Olsen HS, Rosen CA;  
XX PF Ritten SM, Shi Y, Soppet DR, Wei Y, Young P;  
XX XX  
XX WPT: 1999-004069/25.  
XX PF P 650W; Y19656.  
XX XX  
XX XX New isolated human genes and the secreted polypeptides they encode  
XX XX  
XX PR claim 3; Page 470; 744pp; English.  
XX XX  
XX XX The specification describes cDNA sequences (X61422-X61470) encoding human  
XX XX secreted proteins (Y19660). The polypeptides and their  
XX XX corresponding secreted polypeptides are useful for prevention, treatment  
XX XX of, or amelioration of, medical conditions, e.g., by protein or gene therapy.  
XX XX patholological conditions can also be diagnosed by determining the amount  
XX XX of the polypeptides in a sample or by determining the presence of  
XX XX mutations in the polypeptide genes. Specific uses are described for each  
XX XX of the polypeptides, based on which tissues they are most highly  
XX XX expressed in, and include developed products for the diagnosis or  
XX XX treatment of cancer, tumors, neurodegenerative disorders, leukemias,  
XX XX abnormalities and fetal deficiencies, blood disorders, leukemias,  
XX XX disorders of the immune system, autoimmune diseases, hepatic and renal  
XX XX diseases, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's  
XX XX and connective disorders, schizophrania, prostate disease, obesity,  
XX XX disorders involving osteoclasts such as osteoporosis, arthritis or  
XX XX malnutrition, diseases of testes, lung or thymus, digestive/endocrine  
XX XX disorders, infections and AIDS. The polypeptides are also used to  
XX XX identify their binding partners.  
XX XX  
XX PR Sequence 1049 bp; 457 A; 178 C; 213 G; 328 T; 3 other;  
XX XX

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Query Match          12.4%; Score 32.4; DB 20; Length 1049;
Best Local Similarity 53.7%; Pred. No. 2.1;
Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 92 atttgaatgagatgaatgaacgt aaagatgcatatttaataaagacatagatgaacaa 151
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 ATTGAAACCGAGGAAATAGGAAACAGAGTAAACCAATAAAGCAAAACATGAATTAAACA 81

QY 152 taagatccatctctgrratcccttatacagatatttttaaaatataatattccagaaat 211
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 CTCGTGTAGATGAGTCAAGTCACTTAAAGAGCGCTTTTTCCTTTTAACTTAGAGCCCTT 21

QY 212 aga 214
      |||
DB 20 AGA 18

RESULT 11
Q48463
ID Q48463 standard: DNA; 3792 bp.
XX
AC Q48463;
XX
DT 18-MAR-1994 (first entry)
XX
DE Plasmid pG-hes4 containing ts replication system.
XX
KW Temperature sensitive replication; antibiotic resistance marker gene;
KW site-specific recombination; chromosomal integration; inactivation;
KW heterologous gene expression; thermosensitive plasmid; ds.
XX
OS Synthetic.
XX
PN W09318164 A.
XX
ID 16-SEP-1993.
XX
FE 12-MAR-1993; 93W0-FR00248.
XX
PR 14-MAR-1992; 92FR-0003034.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Gross A. Maquin E;
XX
PS WP1: 1993-303478/48.
XX
PT New bacterial plasmid contg. heat sensitive replication system
PT and marker gene, opt. capable of chromosomal integration, used to
PT inactivate specific gene or introduce heterologous gene
XX
PS Example 2; Fig 9; 73pp; French.
XX
CC Plasmid pK12 (Appl. Environ. Microbiol., 48: 726 (1984)) contg. two
CC antibiotic resistance marker genes was subjected to mutagenesis with
CC hydroxylamine. A heat stable mutant was isolated (coding for a heat
CC sensitive RepA - see Q48466 and Q48467), cut with ClaI and HpaII and
CC the 3340bp fragment lacking the ts resistance gene was ligated to a
CC 445bp PvuII fragment of phagescript SK+ containing a multicloning
CC site T7 and T3 promoters and sequencing primer binding sites. The
CC resulting plasmid was designated pVE6004 (or pG-hes4 - Q48463). It
CC is thermosensitive in all hosts tested, including E.coli, and must be
CC maintained at 28 deg.C.
XX
S0 Sequence 3792 bp; 1249 A; 552 C; 742 G; 1249 T; 0 other;

Query Match          12.3%; Score 32.2; DB 14; Length 3792;
Best Local Similarity 56.0%; Pred. No. 3.4;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 10 aaatcaatgaatttcaattctctgttttttaatgaacatgatatataagatptttaa 69

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DB 1699 atatttaagtagctttattattattttttttatgattacaatgataactaatttataaa 1758
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 70 gactcttaatttaacgttttttgaatgaatctatgaatgaatgaacatgaag 118
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1759 attatttatttggatgttttttaaatgagttgatttcaatgatacgaataaaag 1807
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
Q48464
ID Q48464 standard: DNA; 5234 bp.
XX
AC Q48464;
XX
DT 18-MAR-1994 (first entry)
XX
DE Plasmid pG-hes5 containing ts replication system.
XX
KW Temperature sensitive replication; antibiotic resistance marker gene;
KW site-specific recombination; chromosomal integration; inactivation;
KW heterologous gene expression; thermosensitive plasmid; ds.
XX
OS Synthetic.
XX
PN W09318164-A.
XX
ID 16-SEP-1993.
XX
FE 12-MAR-1993; 93W0-FR00248.
XX
PR 14-MAR-1992; 92FR-0003034.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Gross A. Maquin E;
XX
PS WP1: 1993-304478/38.
XX
PT New bacterial plasmid contg. heat sensitive replication system -
PT and marker gene, opt. capable of chromosomal integration, used to
PT inactivate specific gene or introduce heterologous gene
XX
PS Example 2; Fig 10; 73pp; French.
XX
CC Plasmid pK12 (Appl. Environ. Microbiol., 48: 726 (1984)) contg. two
CC antibiotic resistance marker genes was subjected to mutagenesis with
CC hydroxylamine. A heat stable mutant was isolated (coding for a heat
CC sensitive RepA - see Q48466 and Q48467), cut with ClaI and HpaII and
CC the 3340bp fragment lacking the ts resistance gene was ligated to a
CC 445bp PvuII fragment of phagescript SK+ containing a multicloning
CC site T7 and T3 promoters and sequencing primer binding sites. The
CC resulting plasmid was designated pVE6004 (or pG-hes4 - Q48463).
CC To facilitate cloning in E.coli, the 1.4kb Aval-AluNI fragment of
CC pK122 (containing the origin of replication) was inserted into
CC SmaI cleaved pG-hes4 to give pG-hes5 (Q48464). The pK122 ORI
CC allows maintenance of the plasmid in E.coli at 37 deg.C, while the
CC heat-sensitive ORI allows maintenance at 28 deg.C in gram positive
CC bacteria.

```







GenCore version 4.5  
Copyright (c) 1994-2000 CompuGen Ltd.

em nucleotide : nucleotide search, using sw model

Run on: April 11, 2001, 15:40:22 : Search time 3344.34 Seconds  
(without alignments)  
590.882 Million cell updates/sec

Title: US-09-490-609b-317  
Perfect score: 282  
Sequence: 1 aacccaaacacgaatcgaat.....ctttgcggaatgaataac 282

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 7991742 seqs, 450474858 residues

Total number of hits satisfying chosen parameters: 1598484

Minimum low seq length: 0

Maximum low seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST :

1: ab\_est1: \*  
2: ab\_est2: \*  
3: ab\_est3: \*  
4: ab\_est4: \*  
5: ab\_est5: \*  
6: ab\_est6: \*  
7: ab\_est7: \*  
8: ab\_est8: \*  
9: ab\_est9: \*  
10: ab\_est10: \*  
11: ab\_est11: \*  
12: ab\_est12: \*  
13: ab\_est13: \*  
14: ab\_est14: \*  
15: ab\_est15: \*  
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42: em\_est42: \*  
43: em\_est43: \*

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 185: em\_estp84:\*  
 186: em\_estp85:\*  
 187: em\_estp86:\*  
 188: em\_estp87:\*  
 189: em\_estp88:\*

190: qb\_qss25:\*  
 191: qb\_qss26:\*  
 192: qb\_qss27:\*  
 193: qb\_qss28:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	% Match	Query Length	DB	ID	Description
1	261.2	92.6	886	12	AA849214	AA849214 EST191981
2	182.4	64.7	683	96	AA914510	AA914510 m154009.y
3	182.4	64.7	710	109	BE541615	BE541615 601240620
4	182.4	64.7	645	16	AI114976	AI114976 a141001.y
5	182.4	64.7	829	29	AI051342	AI051342 AI051342
6	181.4	64.3	448	7	AA466427	AA466427 v080101.1
7	181.4	64.3	598	147	W66873	W66873 m196408.1
8	181.4	64.3	669	147	W66821	W66821 m196408.1
9	181.4	64.3	750	87	AA214226	AA214226 m011109.y
10	180.8	64.1	522	26	AI193572	AI193572 m011109.y
11	180.8	64.1	651	2	AA097695	AA097695 m011109.y
12	180.8	64.1	803	29	AI080764	AI080764 AI080764
13	180.8	64.1	825	29	AI079797	AI079797 AI079797
14	180.6	64.0	571	9	AA592415	AA592415 v024006.1
15	180.4	64.0	495	108	BE448424	BE448424 m189005.y
16	179.8	63.8	418	88	AA242556	AA242556 m011109.y
17	179.8	63.8	804	29	AI080259	AI080259 AI080259
18	179.6	63.7	510	11	AA711176	AA711176 v118300.1
19	179.2	63.5	528	111	BE555109	BE555109 m111000.y
20	178.8	63.4	407	88	AA258756	AA258756 m023004.y
21	178.4	63.3	531	109	BE554226	BE554226 m14104.y
22	178.4	63.3	656	87	AA229447	AA229447 m099004.y
23	177.6	62.7	825	29	AI079644	AI079644 AI079644
24	176.8	62.7	442	6	AA489556	AA489556 m024005.y
25	176.4	62.6	456	89	AA207440	AA207440 m024005.y
26	175.2	62.1	490	10	AA657114	AA657114 v126005.1
27	173.4	61.5	815	29	AI067155	AI067155 AI067155
28	173.4	61.5	877	29	AI051708	AI051708 AI051708
29	172.4	61.5	908	147	BE591687	BE591687 m166409
30	172.4	61.5	520	10	AA688728	AA688728 m024005.y
31	172.4	61.5	643	4	AA221446	AA221446 m024005.y
32	172.4	61.5	748	29	AI035650	AI035650 AI035650
33	171.8	60.9	988	109	BE554309	BE554309 m140407.y
34	171.8	60.9	988	148	BE580446	BE580446 m11003.1
35	170.4	60.4	563	9	AA596869	AA596869 v021103.1
36	169.2	60.0	299	138	BE597418	BE597418 m11003.1
37	167.4	59.4	480	29	AI036012	AI036012 AI036012
38	166.2	58.9	601	106	BE291401	BE291401 m01084966
39	166.2	58.9	610	13	AA200085	AA200085 v225105.1
40	166.2	58.9	636	106	BE300681	BE300681 m01084966
41	166.2	58.9	815	29	AI051277	AI051277 AI051277
42	165.2	58.6	714	110	BE574864	BE574864 m0110843
43	164.4	58.3	514	8	AA499997	AA499997 v192012.1
44	164.4	58.3	519	10	AA556480	AA556480 m11007.1
45	159.4	56.5	923	29	AI079072	AI079072 AI079072

ALIGNMENTS

RESULT	1	AA849214	886 bp	EST
AA849214	1	AA849214	886 bp	40 APR 1999
LOCUS	1	AA849214	886 bp	40 APR 1999
DEFINITION	1	AA849214	886 bp	40 APR 1999
ACCESSION	1	AA849214	886 bp	40 APR 1999
VERSION	1	AA849214	886 bp	40 APR 1999
KEYWORDS	1	AA849214	886 bp	40 APR 1999
SOURCE	1	AA849214	886 bp	40 APR 1999













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(1)ab_host="phlOR"
Vector: pME185-FL3; Site_1: DraIII (CACTGCTG);
Note: Vector: pME185-FL3; 1st strand cDNA was primed
Site_2: DraIII (CACTGCTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGCGCTTTTTTTTTTTT];
with an oligo(dT) primer [ATGCGCTTTTTTTTTTTT];
Double-stranded cDNA was ligated to a DraIII adaptor
[TTTGGTGGCTTCTACCTG] digested and cloned into distinct DraIII
sites of the pME185-FL3 vector (5' site CACTGCTG, 3' site
CACTGCTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
> 5 kb. Library constructed by Dr. Samio Suckow.

```

(University of Tokyo, Institute of Medical and Pharmaceutical Sciences, 1-1-1, Yoiyogi, Tokyo 113, Japan)  
Custom primers for sequencing: 5' end primer  
CTCTCTCTTAAAAAGTTCG and 3' end primer  
CGACCGGAGCTGACAAA. n = 2 of pairs  
4 1.22 c 1.46 a 1.25 f

[illegible]

0.51 bp mRNA  
EST 25-067-1996  
10.0 nt full length mouse embryo 13 dpc, 10666014 Mus musculus  
clone BAC#F53627 5' similar to db:X62940 M.musculus 1387,22  
mouse), mRNA sequence.  
95  
95, 1 51:1643362

mouse.

scotals; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Cyprinodontiformes; Poeyaceae; Muridae; Murinae; Mus;  
Mus 1 to 631)  
Allen, M., Bowles, M., Dietrich, N., Dubucque, J.,  
S.M., Hillier, L., Allen, M., Le M., Martin, J., Morris, M.,  
S., Kudabak, T., Lucy, M., Le M., Martin, J., Morris, M.,  
emberger, K., Stappert, M., Tan, F., Underwood, K., Moore, R.,  
ton, B., Wylie, L., Leonon, G., Soares, B., Wilson, R. and  
Stob, R.

Flushed-HMI Mouse EST Project  
Flushed (1996)  
Mitra M/Mouse EST Project  
HMI Mouse EST Project  
ation University School of Medicine,  
Forest Park Parkway, Box 8501, St. Louis, MO 63108  
414 286 1800  
414 286 1810

mouse@watson.wustl.edu  
clone is available royalty-free through HMI ; contact the  
Consortium ([international.hmi.org](mailto:international.hmi.org)) for further information.

[illegible]

157 d 168 s 176 q 148 t

[illegible]

2. A0000764 803 bp mRNA EST  
A0000764 Suscra mouse brain mick Mus musculus cDNA clone MN-1  
5' mRNA sequence.

4. A0000764  
A0000764.1 G1:G08518  
EST.  
mouse mouse.  
Mus musculus  
Fukuyama; Metazoa; Chordata; Vertebrata; Euteleostei  
Mammalia; Euteleostei; Rodentia; Sciurognathi; Muridae; Murinae

5. I (Chases, 1 to 803)  
hashimoto,K., Kusuda,J., Tanuma,K., Ho,A., Hirata,K., Toyoda,  
Suzuki,Y., Sasaki,M., and Saitoh,S.  
Isolation of full-length cDNA clones from a mouse brain cDNA  
library made by oligo-capping method  
unpublished (1999)  
Contact : Katsuyuki Hashimoto  
National Institute of Infectious Diseases  
4-1-1, Toyama 2-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
Email: khashimoto@nii.ac.jp  
URL: <http://www.niid.ac.jp/4-1-1/department/>  
GenBank/GenBank  
1. 2003  
/contamin "Mus musculus"  
/strain "mick/mk."

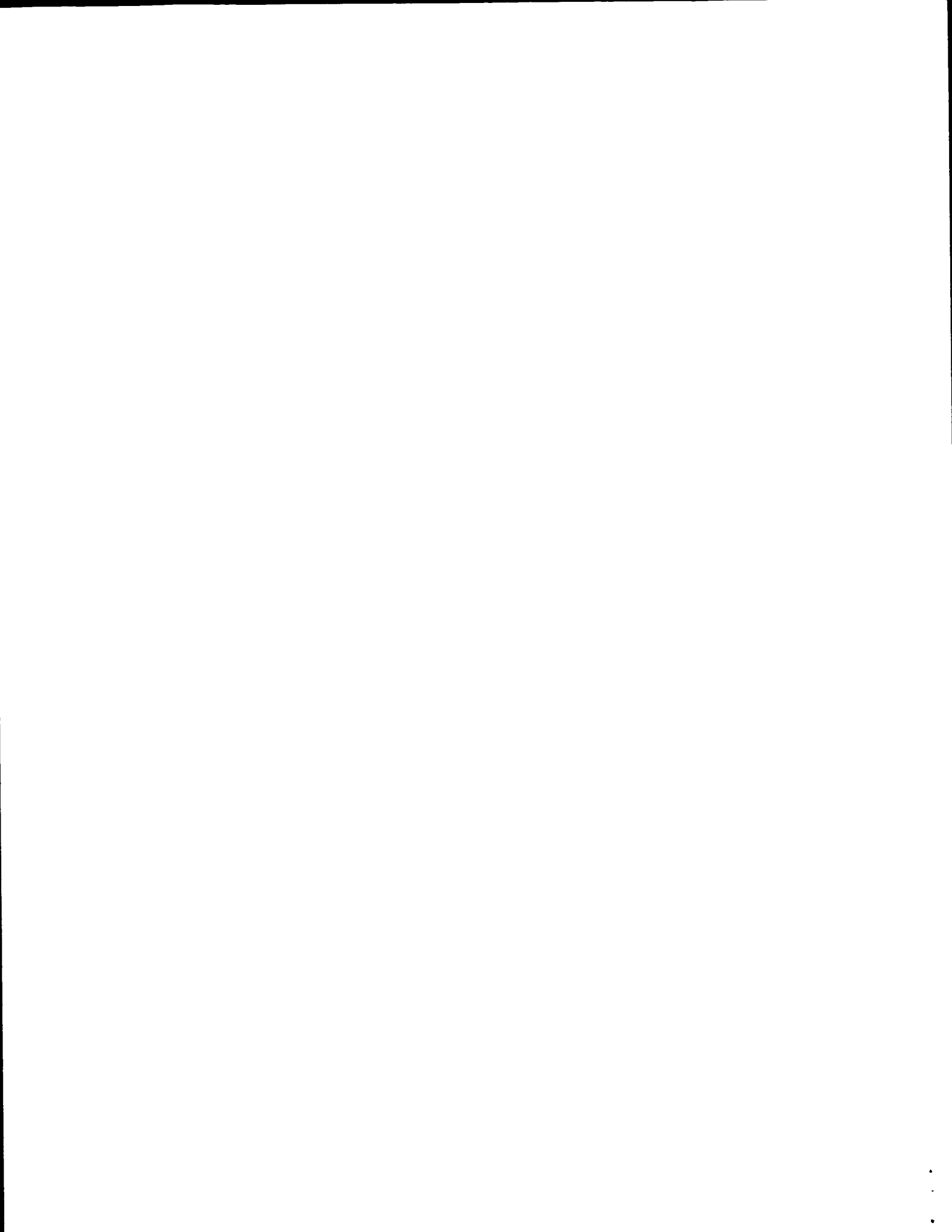
Source











GenCore version 4.5  
Copyright (c) 1993 - 2000 Compuware Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2001, 17:53:19 ; Search time 4464.91 Seconds  
(without alignments)  
299.162 Million cell updates/sec

Title: us-09-490-609b-318

Perfect score: 261

Sequence: 1 aaaaaaqaqaatcaatgaa.....taagcctctattaaaaa 261

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 118134 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 260900000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenBank:

1: gb\_ba1:\*  
2: gb\_ba2:\*  
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4: gb\_ov:\*  
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6: gb\_pl1:\*  
7: gb\_pl2:\*  
8: gb\_pr1:\*  
9: gb\_pr2:\*  
10: gb\_pr3:\*  
11: gb\_ro:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: em\_hun:\*  
15: em\_hum1:\*  
16: em\_hum2:\*  
17: em\_in:\*  
18: em\_om:\*  
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29: gb\_hq1:\*  
30: gb\_hq2:\*  
31: gb\_in1:\*  
32: gb\_in2:\*  
33: gb\_ba1:\*  
34: gb\_ba2:\*  
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36: em\_hum4:\*  
37: gb\_pr4:\*  
38: gb\_hq3:\*  
39: gb\_hq4:\*  
40: gb\_hq5:\*  
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42: gb\_hq7:\*  
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53: gb\_hq12:\*  
54: gb\_hq13:\*  
55: gb\_hq14:\*  
56: gb\_in3:\*  
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59: gb\_hq17:\*  
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64: em\_hum6:\*  
65: gb\_hq18:\*  
66: gb\_hq19:\*  
67: gb\_hq20:\*  
68: gb\_hq21:\*  
69: gb\_hq22:\*  
70: gb\_hq23:\*  
71: gb\_vl1:\*  
72: gb\_vl2:\*  
73: gb\_ba3:\*  
74: em\_hq8:\*  
75: em\_hq9:\*  
76: em\_hq10:\*  
77: gb\_pr6:\*  
78: gb\_pr7:\*  
79: gb\_sts1:\*  
80: gb\_sts2:\*  
81: gb\_pat1:\*  
82: gb\_pat2:\*  
83: em\_hq0:\*  
84: gb\_hq24:\*  
85: gb\_pr8:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	bp	tp	Description
1	253.6	97.2	1594	11	R38812A	X69621 R. norvegicus
2	253.6	97.2	1605	11	AB037934	AB037934 Rattus no
3	253.6	97.2	6125	11	PAT95902	U01662 P. patens norv
4	252	96.6	1594	11	KAT3BP1	U28467 Rat mRNA fo
5	139	49.8	1573	11	EM028947	U28937 Mus musculu
6	87.6	37.6	1216	21	ES9277	U09277 cDNA insert
7	67.4	25.8	1109	11	U86217	U86217 Mus musculu
8	40.6	15.6	96258	67	AL161729	AL161729 Homo sapi
9	40.6	15.6	120314	37	AL133338	AL133338 Human DNA
10	40.6	15.6	171777	68	AL356122	AL356122 Homo sapi
11	40	15.3	1394	3	AB035446	AB035446 Bos tauru
12	40	15.3	14499	1	AF002123	AF002123 Hreoplasm
13	38.8	14.9	172027	52	AC026090	AC026090 Homo sapi
14	38.4	14.7	105891	8	AC004850	AC004850 Homo sapi
15	38.4	14.7	191956	42	AC018911	AC018911 Homo sapi
16	38.2	14.6	177575	57	AC064846	AC064846 Homo sapi
17	38	14.6	70644	57	AC068593	AC068593 Homo sapi
18	38	14.6	154524	38	AC011660	AC011660 Homo sapi
19	38	14.6	199987	53	AC026982	AC026982 Homo sapi
20	37.8	14.5	180534	53	AC026759	AC026759 Homo sapi
21	37.6	14.4	145888	58	AC073219	AC073219 Homo sapi























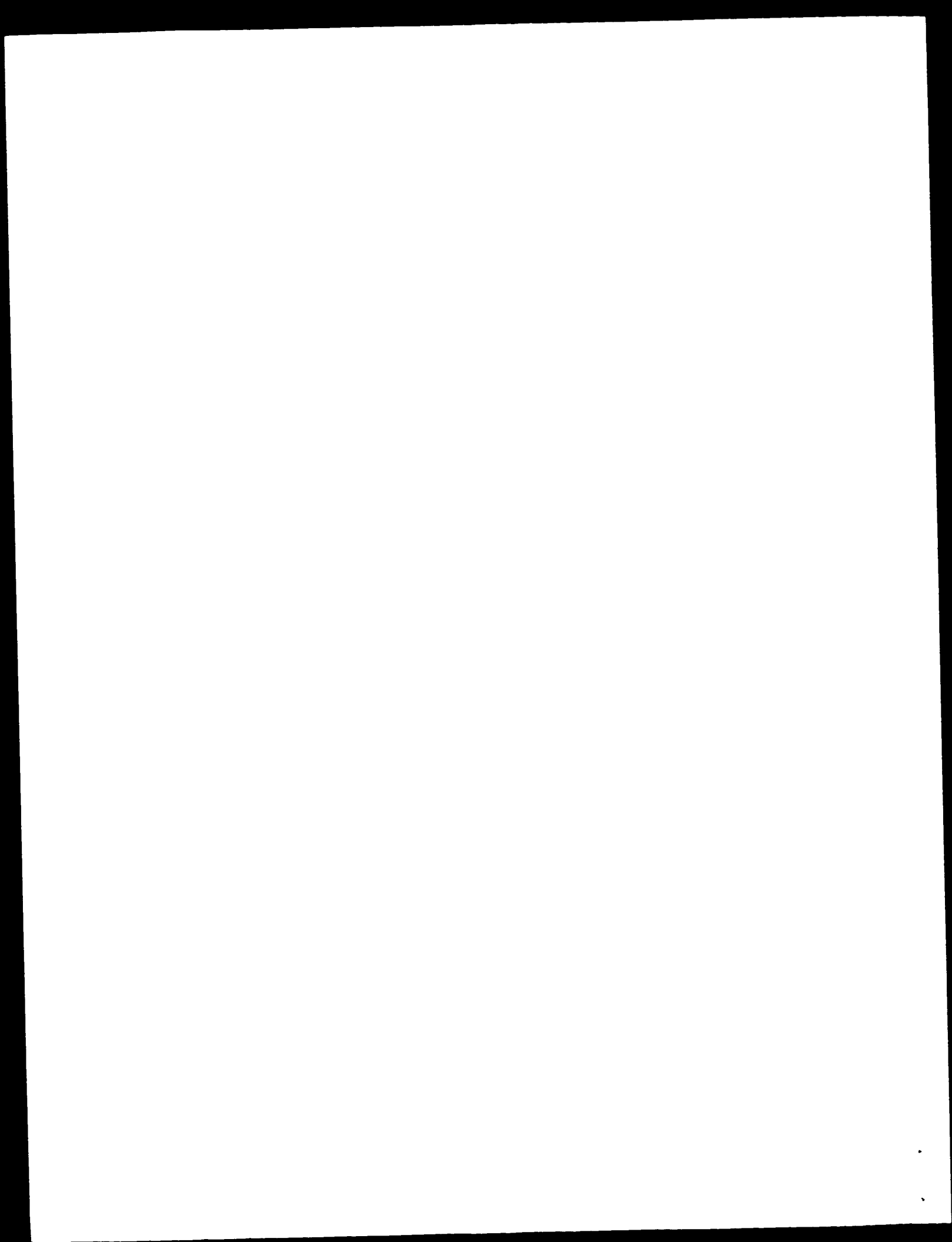














us-09-490-609b-318.rst

Thu Apr 12 10:22:23 2001

117: em\_ost161:\*

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121: em\_ost170:\*

122: em\_ost171:\*

123: em\_ost172:\*

124: em\_ost173:\*

125: em\_ost174:\*

126: em\_ost175:\*

127: em\_ost176:\*

128: em\_ost177:\*

129: em\_ost178:\*

130: em\_ost179:\*

131: em\_ost180:\*

132: em\_ost181:\*

133: em\_ost182:\*

134: em\_ost183:\*

135: em\_ost184:\*

136: em\_ost185:\*

137: em\_ost186:\*

138: em\_ost187:\*

139: em\_ost188:\*

140: em\_ost189:\*

141: em\_ost190:\*

142: em\_ost191:\*

143: em\_ost192:\*

144: em\_ost193:\*

145: em\_ost194:\*

146: em\_ost195:\*

147: em\_ost196:\*

148: em\_ost197:\*

149: em\_ost198:\*

150: em\_ost199:\*

151: em\_ost200:\*

152: em\_ost201:\*

153: em\_ost202:\*

154: em\_ost203:\*

155: em\_ost204:\*

156: em\_ost205:\*

157: em\_ost206:\*

158: em\_ost207:\*

159: em\_ost208:\*

160: em\_ost209:\*

161: em\_ost210:\*

162: em\_ost211:\*

163: em\_ost212:\*

164: em\_ost213:\*

165: em\_ost214:\*

166: em\_ost215:\*

167: em\_ost216:\*

168: em\_ost217:\*

169: em\_ost218:\*

170: em\_ost219:\*

171: em\_ost220:\*

172: em\_ost221:\*

173: em\_ost222:\*

174: em\_ost223:\*

175: em\_ost224:\*

176: em\_ost225:\*

177: em\_ost226:\*

178: em\_ost227:\*

179: em\_ost228:\*

180: em\_ost229:\*

181: em\_ost230:\*

182: em\_ost231:\*

183: em\_ost232:\*

184: em\_ost233:\*

185: em\_ost234:\*

186: em\_ost235:\*

187: em\_ost236:\*

188: em\_ost237:\*

189: em\_ost238:\*

191: qb\_oss21:\*

192: qb\_oss22:\*

193: qb\_oss23:\*

194: qb\_oss24:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	bp	Description
1	144.2	51.0	710	25	A1787293
2	142.2	50.7	773	16	A1118289
3	140.2	49.8	555	18	A1265282
4	130.2	49.8	552	18	A1265282
5	130.2	49.8	552	18	A1265282
6	128.4	49.2	749	17	A1173524
7	126.8	48.6	746	25	A1786989
8	124.6	47.4	751	17	A1173524
9	121.2	46.4	531	17	A1195928
10	120.4	46.1	815	17	A1194750
11	118.6	45.4	506	25	A1786885
12	118.6	45.4	532	17	A1195928
13	117.6	45.1	519	40	A1114406
14	117.6	45.1	805	25	A1789754
15	102.2	49.2	468	4	AA244771
16	97.8	47.5	506	17	A1173524
17	96.8	47.1	464	25	A1787307
18	87.8	43.3	456	4	AA255065
19	87.8	43.3	456	4	AA255065
20	86.2	42.4	432	16	AA269448
21	86.2	42.4	432	16	AA269448
22	84.4	42.0	497	18	A1265162
23	83.6	42.0	498	29	AA028322
24	80.4	40.8	495	17	A1195266
25	68.8	26.4	470	17	A1195266
26	52.2	19.9	331	3	AA212829
27	51.2	19.6	304	4	AA244541
28	51.2	19.6	306	29	AA028322
29	46.8	17.9	387	13	AA059861
30	46.6	17.9	387	13	AA059861
31	41.2	15.8	768	190	CNS000000
32	40.6	15.6	516	16	A1091448
33	40.6	15.6	646	24	A1741521
34	40.4	15.3	827	190	CNS000000
35	40.4	15.3	524	135	BE750828
36	40.4	15.3	524	135	BE750828
37	37.8	14.5	811	190	CNS000000
38	37.6	14.4	408	149	AA090757
39	37.6	14.4	429	17	A1259608
40	37.4	14.3	765	27	A1789446
41	37.2	14.3	448	24	A1753791
42	37.2	14.3	479	91	AA012997
43	37.2	14.3	479	91	AA012997
44	37.2	14.3	479	91	AA012997
45	37.2	14.3	479	91	AA012997

# ALIGNMENTS

RESULT 1

A1787293/

LOCUS

DEFINITION

IMAGE:1924171.37 similar to SW:SM00\_MOUSE\_Q6474 SINE-SERPENT MARKER

PROTEIN 40 % mRNA sequence.

ACCESSION

VERSION

KEYWORDS

A1787293

3158110 x1 Squape mouse liver mRNA

IMAGE:1924171.37 similar to SW:SM00\_MOUSE\_Q6474 SINE-SERPENT MARKER

PROTEIN 40 % mRNA sequence.

ACCESSION

VERSION

KEYWORDS

EST

02 JUL 1999

mus musculus cDNA clone

IMAGE:1924171.37 similar to SW:SM00\_MOUSE\_Q6474 SINE-SERPENT MARKER

PROTEIN 40 % mRNA sequence.

ACCESSION

VERSION

KEYWORDS















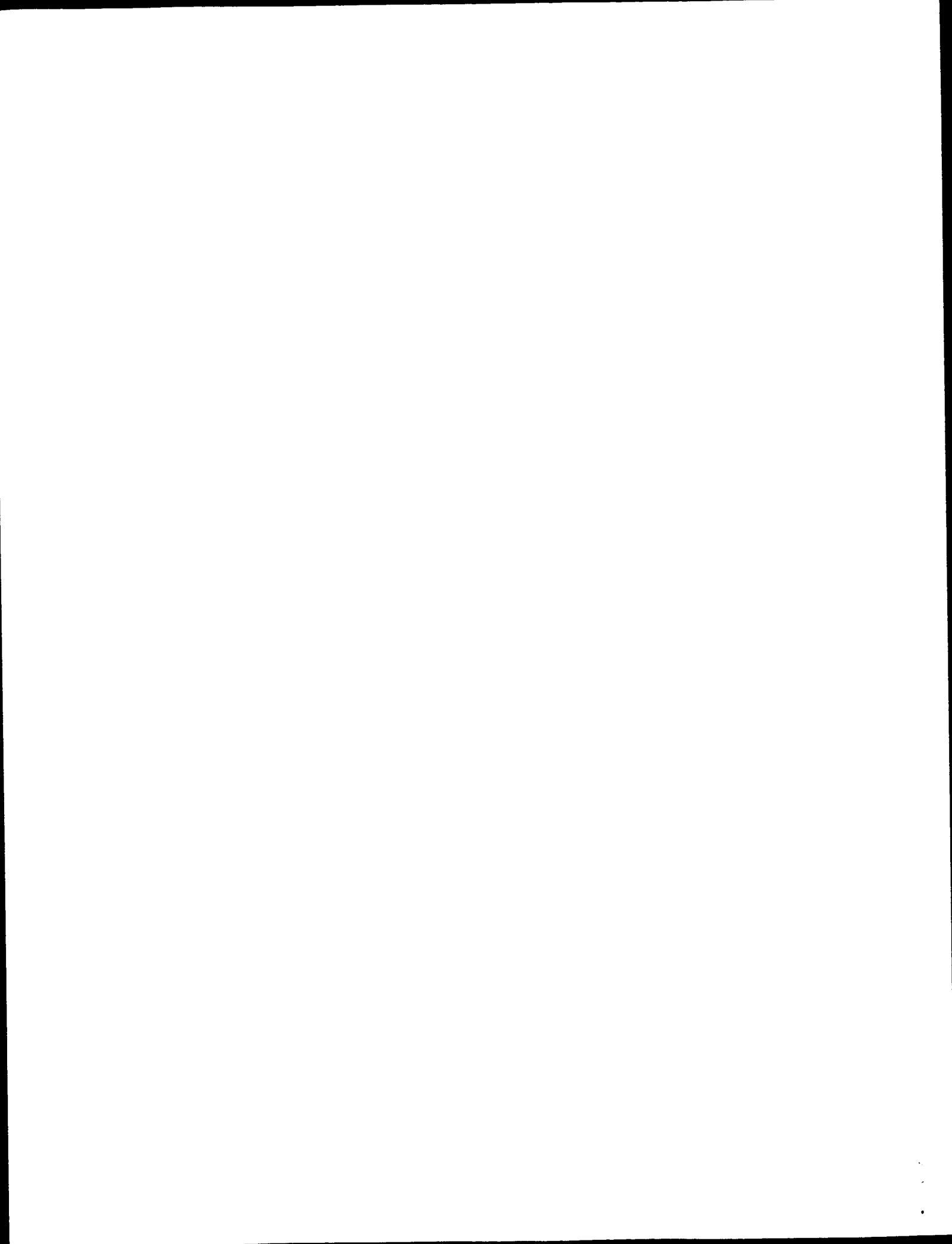




SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:  
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus:  
1 (bases 1 to 468)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucuba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stępień, M., Tan, F., Underwood, K., Moore, B.,  
Theising, R., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through INL: contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MCL:419062  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 467.

FEATURES  
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/note="Vector: p7710-Pac (Pharmacia) with a modified  
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was primed with a Not 1 - oligo(dT) primer [5];  
TGTTACCTAATCGAGTCGAGCGGCGGCAACTTTTTTTTTTTT 3' ];  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not 1 and cloned into the Not 1  
and Eco RI sites of the modified p1713 vector. Library  
constructed and normalized by Bento Soares and M.Fatima  
Bonaldi."

BASE COUNT 135 a 73 c 111 q 149 t  
ORIGIN  
Query Match 49.2% Score 102.2; Db 4; Length 468;  
Best local Similarity 78.0%; Pred. NO. 1.2e-16;  
Matches 181; Conservative 9; Mismatches 29; Indels 22; Gaps 4;  
QY 1 aatggaagaatcaatgaatttcaactctg-tttttttaaagcaatgaatata 59  
Db 257 AAGCGACGCGAATCAATGAACCTTCAATTAGTTTTTTTAAAGGCGTGATATTATA 316  
QY 60 gatatgaataactgttttaattacactttttgaattgaactga gaaataaactaaag 118  
Db 317 GCAATGTTAA---GCTTAATTACATCTTTCATTCGGCTCTGGTTGAATAAAGCTAGCG 374  
QY 119 catggaatattaaagaacatataatgaacataaactccatctctgaattcccttata 178  
Db 374 CATAGCATATTATGAATAGTGT-----CATGCGCTGATTCCTTATT 416  
QY 179 ggaatatttttaagtttaagtattccacacagaatgaatgaatgaattttta 240  
Db 417 TAGAATTTTTTAAGGTGAGAGATTTCCTCCAGAGAAATGCAAGATGGTTTTS 468  
Search completed: April 11, 2001, 15:40:40  
Job time: 13503 sec

































us-09-490-609b-384.rge

Thu Apr 12 10:22:28 2001





TITLE Direct Submission  
 JOURNAL Submitted (on the 1999) Genome Sequencing Center, Washington  
 University, Seattle, WA, U.S.A. 1441 Park Parkside, Seattle, WA, U.S.A.  
 MO 68108, USA  
 COMMENT on Jan 16, 2000 this sequence version replaced nt.7659475.

\*\*\*\*\* Genome Center \*\*\*\*\*  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 29 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1313: contig of 1413 bp in length  
 1414: gap of unknown length  
 1414 2619: contig of 1296 bp in length  
 2620 2712: gap of unknown length  
 2720 3887: contig of 1168 bp in length  
 3888 3987: gap of unknown length  
 3988 5295: contig of 1308 bp in length  
 5296 5395: gap of unknown length  
 5396 6572: contig of 1177 bp in length  
 6573 6673: gap of unknown length  
 6674 8101: contig of 1429 bp in length  
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 10077 10173: gap of unknown length  
 10174 12439: contig of 2263 bp in length  
 12440 12539: gap of unknown length  
 12540 14893: contig of 2354 bp in length  
 14894 14993: gap of unknown length  
 14994 17493: gap of unknown length  
 17496 21722: contig of 4127 bp in length  
 21723 23823: gap of unknown length  
 23824 27619: contig of 5797 bp in length  
 27620 27721: gap of unknown length  
 27722 31491: contig of 4772 bp in length  
 31492 31592: gap of unknown length  
 31593 36801: contig of 5210 bp in length  
 36802 43269: contig of 6368 bp in length  
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 43370 45415: contig of 6046 bp in length  
 45416 45515: gap of unknown length  
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 55006 62000: contig of 6895 bp in length  
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 62101 69529: contig of 7825 bp in length  
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 122896 134376: contig of 11382 bp in length  
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 Location/Qualifiers

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 M: 253 209, Descriptive 0, Mismatches 12, Indels 6, Gaps 4

[illegible]







DB 188853 AAACCTTCAGTTCCTGTAAGAGTACGATGTAACATGCTGCTGATTCAGACAGCTG 188794

QY 297 30 296

DB 188793 AA 188792

RESULT 8

AC022940

LOCUS

DEFINITION

AC022940

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1333: contig of 1333 bp in length  
1434 1434: gap of 100 bp  
1434 3122: contig of 1689 bp in length  
3123 3222: gap of 100 bp  
3223 5217: contig of 1995 bp in length  
5218 5317: gap of 100 bp  
5318 8117: contig of 2800 bp in length  
8118 8217: gap of 100 bp  
8218 11178: contig of 2961 bp in length  
11179 11278: gap of 100 bp  
11279 15255: contig of 2477 bp in length  
15256 15355: gap of 100 bp  
15356 18989: contig of 3634 bp in length  
18990 19089: gap of 100 bp  
19090 24048: contig of 4459 bp in length  
24049 24148: gap of 100 bp  
24149 28201: contig of 4053 bp in length  
28202 28301: gap of 100 bp  
28302 33551: contig of 5250 bp in length  
33552 39489: contig of 6338 bp in length  
39490 40089: gap of 100 bp  
40090 45900: contig of 5811 bp in length  
45901 46000: gap of 100 bp  
46001 52633: contig of 6633 bp in length  
52634 52733: gap of 100 bp  
52734 59964: contig of 7231 bp in length  
59965 60064: gap of 100 bp  
60065 69189: contig of 9125 bp in length  
69190 69299: gap of 100 bp  
69300 80945: contig of 11646 bp in length  
80946 81045: gap of 100 bp  
81046 92964: contig of 11929 bp in length  
92965 93064: gap of 100 bp  
93065 107886: contig of 14922 bp in length  
107887 107986: gap of 100 bp  
107987 122024: contig of 14038 bp in length  
122025 122124: gap of 100 bp  
122125 137999: contig of 15875 bp in length  
138000 138099: gap of 100 bp  
138100 154878: contig of 16779 bp in length  
154879 154978: gap of 100 bp  
154979 172438: contig of 17450 bp in length  
172439 172528: gap of 100 bp  
172529 191944: contig of 19416 bp in length.

#### FEATURES

Location/Qualifiers  
1..191944  
/organism "Homo Sapiens"  
/db\_xref "taxon:9606"  
/chromosome "17"  
/map "17"  
/clone="RP11-341P19"  
/clone\_lib="RP11 Human Male BAC"  
1..1333  
/note "assembly\_fragment"  
1434..3122  
/note "assembly\_fragment"  
3123..5217  
/note "assembly\_fragment"  
5318..8117  
/note "assembly\_fragment"  
8218..11178  
/note "assembly\_fragment"  
11279..15255  
/note "assembly\_fragment"  
15356..18989  
/note "assembly\_fragment"  
19090..24048  
/note "assembly\_fragment"  
24149..28201  
/note "assembly\_fragment"

#### Source

Center: Whitehead Institute/ MIT Center for Genome Research,  
Web site: <http://www.mit.edu>  
Contact: SequencingSubmissions@genome.wi.mit.edu

#### Project Information

Center project name: 16339  
Center clone name: 341P\_19  
Sequencing vector: M13, M7815; 100% of reads  
Chemistry: dye-terminator Big Dye; 100% of reads  
Assembly program: phrap; version 0.9603i  
Consensus quality: 17924 bases at least Q19  
Consensus quality: 19575 bases at least Q20  
Consensus quality: 18823 bases at least Q20  
Insert size: 160000; average 1p  
Insert size: 189744; sum-of-contigs  
Quality coverage: 4.4 in Q20 bases; average 1p  
Quality coverage: 4.4 in Q20 bases; sum of contigs

\* Ref: this is a 'working draft' sequence. It currently  
\* consists of 23 contigs, the true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.















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GenCore version 4.5

08 nucleotide - nucleotide search, using sw model

Run on: April 11, 2001, 17:56:01 : Search time 4464.91 Seconds  
(without alignments)  
342.719 Million cell updates/sec

File: us-09-490-609b-384  
Project score: 299  
Sequence: 1 aactacacattacatccccc.....tctatattgaagatgaag-299

Scoring table: IDENTITY 80%  
Gapop 10.0 / Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues 2246266  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 209090909  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenBank  
1: qb\_ba1: \*  
2: qb\_ba2: \*  
3: qb\_cmc: \*  
4: qb\_cw: \*  
5: qb\_ph: \*  
6: qb\_p11: \*  
7: qb\_p12: \*  
8: qb\_p13: \*  
9: qb\_p14: \*  
10: qb\_p15: \*  
11: qb\_ro: \*  
12: qb\_sy: \*  
13: qb\_un: \*  
14: qb\_un: \*  
15: cm\_hum1: \*  
16: cm\_hum2: \*  
17: cm\_hum3: \*  
18: cm\_cmc: \*  
19: cm\_cw: \*  
20: cm\_cw: \*  
21: cm\_cw: \*  
22: cm\_ph: \*  
23: cm\_p1: \*  
24: cm\_ro: \*  
25: cm\_sy: \*  
26: cm\_sy: \*  
27: cm\_un: \*  
28: cm\_un: \*  
29: qb\_ha1: \*  
30: qb\_ha2: \*  
41: qb\_ha1: \*  
42: qb\_ha2: \*  
43: cm\_ba1: \*  
44: cm\_ba2: \*  
45: cm\_hum4: \*  
46: cm\_hum4: \*  
47: qb\_p14: \*  
48: qb\_ha3: \*  
49: qb\_ha4: \*  
40: qb\_ha5: \*  
41: qb\_ha6: \*  
42: qb\_ha7: \*  
43: cm\_ha1: \*

44: cm\_ha2: \*  
45: cm\_ha3: \*  
46: cm\_ham5: \*  
47: qb\_p15: \*  
48: qb\_p16: \*  
49: qb\_ha8: \*  
50: qb\_ha9: \*  
51: qb\_ha10: \*  
52: qb\_ha11: \*  
53: qb\_ha12: \*  
54: qb\_ha13: \*  
55: qb\_ha14: \*  
56: qb\_ha15: \*  
57: qb\_ha16: \*  
58: qb\_ha17: \*  
60: cm\_ha4: \*  
61: cm\_ha5: \*  
62: cm\_ha6: \*  
63: cm\_ha7: \*  
64: cm\_hum6: \*  
65: qb\_ha18: \*  
66: qb\_ha19: \*  
67: qb\_ha20: \*  
68: qb\_ha21: \*  
69: qb\_ha22: \*  
70: qb\_ha23: \*  
71: qb\_ha24: \*  
72: qb\_ha25: \*  
73: qb\_ha26: \*  
74: cm\_ha8: \*  
75: cm\_ha9: \*  
76: cm\_ha10: \*  
77: qb\_p16: \*  
78: qb\_p17: \*  
79: qb\_ha27: \*  
80: qb\_ha28: \*  
81: qb\_p18: \*  
82: qb\_ha29: \*  
83: cm\_ha11: \*  
84: qb\_ha30: \*  
85: qb\_ha31: \*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
c	1	245	81.9	857	78	HSRUEA
	2	228.4	76.4	185755	40	AC000581
	3	221.2	74.0	215404	68	AL354497
	4	221.2	74.0	244977	66	AL148890
c	5	193.2	64.6	161456	69	AL391535
	6	193	64.5	122923	66	AF248376
c	7	193	64.5	190579	42	AC018736
	8	193	64.5	191944	50	AC022930
c	9	192	64.2	163250	58	AC069217
	10	185.2	61.9	168223	49	AC021558
c	11	184.4	61.7	200710	42	AC019198
	12	183.6	61.4	590	85	HMB11P
	13	183.6	61.4	952	78	HSRUEA
	14	175.2	58.6	159400	48	CNS0115A
	15	169.4	56.7	979	78	HSRUEA
	16	152.8	51.1	600	85	HMB11P
c	17	151.2	50.6	143093	66	AF234070
	18	146.4	49.0	162703	53	AC027407
c	19	146.4	49.0	176615	68	AL351427
c	20	136.6	45.7	61403	54	AC007459
	21	131.4	43.9	1350	85	HMB11P

Search completed: April 11, 2001, 19:37:35  
Job time: 18488 sec





















DE Lambda 10 Insert encoding human lipocortin.  
 XX  
 KW Antinflammatory; arthritis; allergy; dermatology;  
 KW phospholipase A2 inhibitor; ss.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 1..1092  
 FT /\*tag= a  
 FT sig\_peptide 1..57  
 FT /\*tag= b  
 FT mat\_peptide 58..1089  
 FT /\*tag= c  
 FT misc\_feature 81..111  
 FT /\*tag= d  
 FT /\*label= lipos\_16  
 FT /note= "probe"

PN US5081019-A.

PD 14-JAN-1992.

PF 02-MAY-1990; 90US-0519256.

PR 06-MAR-1985; 86US-0837019.

PR 10-JAN-1985; 85US-0690146.

PR 15-MAR-1985; 85US-0712376.

PR 14-AUG-1985; 85US-0765877.

PR 05-SEP-1985; 85US-0772892.

PR 22-FEB-1989; 86US-0314316.

PR 02-MAY-1990; 90US-0519256.

PA (RIGOS ) BIOGEN INC.

XX Wallner BP, Pepinsky RB;

XX WPI: 1992 24727793.

XX P-PSDB: R2232.

XX Deoxyribonucleic acid encoding lipo-cortinoid polypeptide(s) -  
 PT for producing antinflammatory agents for treating arthritic,  
 PT allergic, dermatologic, ophthalmic and collagen diseases  
 XX  
 PS Disclosure: Fig 4: 56pp; English.  
 XX  
 CC The sequence was obtd. from 14 overlapping clones isolated from a  
 CC cDNA library prepd. from polyA+ mRNA from human macrophage cell line  
 CC 0937. The library, in lambda gt10, was initially screened using  
 CC probes (22,225,22) prepared from the corresponding rat sequence.  
 CC Twenty positive plaques were rescreened and two clones were isolated,  
 CC lambda9-11 and lambda21. Restriction treatments from the clones  
 CC were subcloned to prepare 3 plasmids which were sequenced. A 486 bp  
 CC fragment of one of these plasmids, pL9/26, was used as probe to  
 CC rescreen the original library. Seventy two plaques were isolated  
 CC and analysed by Southern blotting using a c-myc (lipo\_16; tag d) as  
 CC a probe. The 14 clones isolated were sequenced and used to determine  
 CC the full sequence encoding lipocortin. Recombinant lipocortin prepd.  
 CC using the DNA sequence has antinflammatory activity and can be used  
 CC for the treatment of arthritic, allergic, dermatologic, ophthalmic  
 CC and collagen diseases.  
 CC See also Q24217-40 and Q24294.

XX Sequence 1990 PP: 454 A: 291 C: 292 G: 450 T: 0 other;

Query Match 18.1%; Score 50.2; DB 16; Length 1376;

Best local Similarity 65.9%; Pred. No. 4.4e-07;

Mismatches 82; Conserved 0; Mismatches 54; Indels 0; Gaps 0;

XX 140 codonaaagcctacacacatcttcaacatcaaacatcttcaacatcaaacacaa 189  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111

XX 155 codtgaagcctacacatcttcaacatcaaacatcttcaacatcaaacacaa 214  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111  
 XX 190 codaaacacaaagcctgaacacatcttcaacatcttcaacacacacaaatg 249  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111  
 XX 215 taatgaatcaacatcaaacacacacatcttcaacatcttcaacacacacaaatg 274  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111  
 XX 250 codaaagcctgaacacat 265  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111  
 XX 275 caacacacacacacat 290  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111

RESHL 14

XX57357

XX X57357 standard; DNA: 1395 bp.

XX X57357;

XX 26-JUL-1999 (first entry)

XX Human p-40/annexin 1 DNA.

XX p-40; annexin 1; human; MBP; multidrug resistance; antitumor;

XX prevention; cancer treatment; detection; pathogen; therapeutic agent;

XX antifungal agent; plant; resistance; antitumor; antifungal; ss.

XX Homo sapiens.

XX W09921980 A1.

XX 06-MAY 1999.

XX 26-OCT 1998; 98W0-CA00492.

XX 24-OCT 1997; 97CA 2219299.

XX (BYMC ) UNIV MCGILL.

XX Georges E, Wang Y;

XX WPI: 1999 377419/28.

XX P-PSDB: Y08412.

XX Metabolism of annexin multidrug resistance related to annexin

XX proteins

XX Claim 5: Fig 1B-C; 6pp; English.

XX This invention describes a novel human annexin family member, p-40 (also  
 XX known as annexin I) which is a member of the MBP (multidrug resistance)  
 XX gene family, for assessing or modulating MBP in a cell. Antitumor p-40  
 XX sequences are used to prevent MBP in animals, particularly in conjunction  
 XX with cancer treatment. Detecting levels of the p-40 nucleic acid, or  
 XX related RNA, is used to detect cancer (or pathogen) with MBP, or  
 XX susceptibility. P-40 nucleic acid can also be used as a target for  
 XX identifying therapeutic agents, e.g., antitumor agents, and increasing  
 XX the nucleic acid expression in plants may be used to develop specific  
 XX resistance. The products of the invention have antitumor and antifungal  
 XX activity.

XX Sequence 1999 PP: 464 A: 273 C: 298 G: 364 T: 0 other;

Query Match 18.1%; Score 50.2; DB 20; Length 1397;

Best local Similarity 60.9%; Pred. No. 4.4e-07;

Mismatches 92; Conserved 0; Mismatches 54; Indels 0; Gaps 0;

XX 140 codtgaagcctacacacatcttcaacatcaaacatcttcaacatcaaacacaa 189  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111

XX 190 codaaacacaaagcctgaacacatcttcaacatcttcaacacacacaaatg 247  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111

XX 215 taatgaatcaacatcaaacacacacatcttcaacatcttcaacacacacaaatg 249  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111

XX 248 taatgaatcaacatcttcaacacacacacacacacacacacacacacacaa 297  
 ||||| 11111 11111 11111 11111 11111 11111 11111 11111

[illegible]

X		Key	Location/Qualities
H	TLS	64..1099	
F		Zinc <sup>a</sup>	
I		Zn(II) "human lipoprotein"	
N	XN	D54950636_A.	
CX	CX	Z1 A06; 1990.	
CX	CX	10 JAN 1986;	R0DS 0929199.
CX	CX	10-JAN 1986;	R0DS 0929199.
KK	KK	0% SEP 1985;	R0RS 0728942.
KK	KK	14 AUG 1985;	R0DS 0765477.
KK	KK	1% MAR 1985;	R0DS 0712376.
KK	KK	10 JAN 1985;	R0DS 0690146.
XX	XX	(BLD) ) BIOGEN NV.	
XX	XX	Wallner BP, Poplinsky RB, Garwin JL, Schindler JG., Baum KJ,	
YY	YY	W01; 1990 ZY453Z/46.	
YY	YY	P-ESPR; R06560.	
XX	XX	pure treatment of human lipoprotein used for reducing inflammation or for treating arthritis, etc.	
XX	XX	Data source: Fig 4; b1pp; English	
XX	XX	Based on the amino acid sequence of rat phospholipase A <sub>2</sub> inhibitor protein, isolated from the extrahepatic supernatant of rat peritoneal exudate cells, several anti sense oligonucleotides were produced to screen a human cDNA library consisting E. coli cells control human macrophage cDNA sequences inserted into a phage cloning vector. The cDNA sequences can be operatively linked to expression or suppression vectors and used to produce the human lipoprotein-like polypeptide proteins which may also be used as probes to screen libraries for other lipoprotein like peptides.	
CC	CC	The 37 kb protein can be used for reducing inflammation or treating arthritis, all types, dermatologic, ophthalmic and colonic diseases and other diseases involving inflammation processes.	
CC	CC	See also G05M03/25, G06F03/00 and R07B/06_37.	
XX	XX	Sequence 1376 bp, 4'3 A, 271 C; 294 G; 527 T; 0 others:	
S9			
	Query Match	18.19%	Score 50.2; Id 11; Length 1476;
	Best Local Siml arity	60.9%	Prod. No. 4136 07;
	Matches	82; Conservative	0; Mismatches 54; Indels 0; Gaps
QY		130 equivalent at quartet level	equivalent at quartet level
Db		131 equivalent at quartet level	equivalent at quartet level
QY		150 equivalent at quartet level	equivalent at quartet level
Db		21% identical at quartet level	identical at quartet level
QY		250 equivalent at quartet level	equivalent at quartet level
Db		27% identical at quartet level	identical at quartet level
RESULT	13		
Q2 Q216			
Id	Q2 Q216 standard; cDNA; 1376 bp.		
XX	Q2 Q216;		
XX	13 MAY 1992 (first entry)		
XX			

```

AC N60556;
XX 08 AUG-1991 (first entry)
XX
XX Sequence of the cDNA insert of lambda 10 which codes for human
XX lipocortin.
XX
XX Anti-inflammatory agent; steroid medication; arthritis therapy.
XX allergy; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1-1034
XX /**L34 3
XX
XX W08604094-A.
XX
XX 17-JUL-1986.
XX
XX 10-JAN-1986; 86WO-0800027.
XX
XX 05-SEP-1985; 85US-0772892.
XX 10-JAN-1985; 85US-0690146.
XX 15-MAR-1985; 85US-0712376.
XX 14-AUG-1985; 85US-0765877.
XX 10-JAN-1986; 86US-0429199.
XX
XX (Hind ) BIOGEN NV.
XX
XX Wallner BP, Pepinsky BR, Garwin JL, Schindler DG, Huang KS;
XX WPI; 1986-196888/40.
XX P-PSDB; P41524.
XX
XX New human lipocortin-like polypeptide(s) - are obt'd. by
XX recombinant DNA techniques and are anti-inflammatory agents
XX without usual side effects
XX
XX Claim 2; Page 75; 113pp; English.
XX
XX A human cDNA library of Escherichia coli cells contg. human
XX macrophage cDNA sequences inserted into a phage cloning vector was
XX screened using antisense oligonucleotide DNA probes corresp. to
XX those regions of rat phospholipase A2 inhibitor protein having
XX minimal nucleotide homology (860561-960564) to obtain a sequence
XX coding for human lipocortin (LC)-like polypeptide.
XX
XX Sequence 1425 BP; 447 A; 262 C; 285 G; 341 T; 0 other;

Query Match. 18.1%; Score 50.2; DB 7; Length 1425.
Best Local Similarity 60.4%; Pred. No. 4.1e-07;
Matches 82. Mismatch 9. Mismatches 54. Indels 5. Gaps 0.

QY 100 caatcaaacctatcaaaatcttcaacatcaaaacatcttcaacatcaaaacatcaaa 165
DB 104 caatcaaacctatcaaaatcttcaacatcaaaacatcttcaacatcaaaacatcaaa 168
QY 166 tcaaaacacaaatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 249
DB 164 tcaatctaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 234
QY 250 caaaacacaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 265
DB 224 caaaacacaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 239

RESULT 10
N82025
ID N82025 standard; DNA: 1355 BP.
XX
XX N82025;
AC N82025;

```

```

XX 22-JUL-1990 (first entry)
XX
XX Fragment containing rat lipocortin gene.
XX
XX Recombinant rat lipocortin; rat abdominal dropsy; ss.
XX
XX Rattus.
XX
XX Key Location/Qualifiers
XX CDS 28..1068
XX /**L34 3
XX /Product lipocortin
XX
XX JF63276497-A.
XX
XX 14-NOV-1988.
XX
XX 08-MAY-1987; 87JP-0112145.
XX
XX 08-MAY-1987; 87JP-0112145.
XX
XX (TAMA ) YAMAMOTO HI; FNAJLM EE.
XX
XX WPI; 1988-46516751.
XX P-PSDB; P82062.
XX
XX Recombinant rat lipocortin -
XX obt'd using gene derived from cells in rat abdominal dropsy
XX
XX Disclosure ; ; Japanese.
XX
XX The coding sequence described in the features is specifically
XX claimed. mRNA was isolated from rat abdominal dropsy cells and cDNA
XX synthesised from it. Probes were synthesised according to the
XX partial amino acid sequence of rat lipocortin (see N82038 and
XX N82377). These were used to isolate plasmids contg the desired
XX sequence of lipocortin cDNA.
XX See also P82063.
XX
XX Sequence 1355 BP; 434 A; 274 C; 402 G; 347 T; 0 other;

Query Match. 18.1%; Score 50.2; DB 9; Length 1355.
Best Local Similarity 60.3%; Pred. No. 4.2e-07;
Matches 82. Mismatch 9. Mismatches 54. Indels 0. Gaps 0.

QY 130 caatcaaacctatcaaaatcttcaacatcaaaacatcttcaacatcaaaacatcaaa 189
DB 131 caatcaaacctatcaaaatcttcaacatcaaaacatcttcaacatcaaaacatcaaa 190
QY 192 tcaaaacacaaatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 249
DB 191 tcaatctaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 244
QY 244 tcaatctaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 250
QY 250 caaaacacaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 265
DB 251 caaaacacaaacatcttcaacatcaaaacatcttcaacatcaaaacatcaaaacatcaaa 266

RESULT 11
N60555
ID N60555 standard; cDNA: 1376 BP.
XX
XX N60555;
AC N60555;
XX
XX 08-AUG-1991 (first entry)
XX
XX Sequence of the cDNA insert of lambda LC which codes for human
XX lipocortin.
XX
XX Anti-inflammatory agent; steroid medication; arthritis therapy;
XX allergy; ds.
XX

```















```

1 TELEPHONE: 403/499-8080
2 TELEFAX: 403/499-8089
3 TELEX: 49617824
4 INFORMATION FOR SEQ ID NO: 1:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 1741 base pairs
7 TYPE: nucleic acid
8 STRANDEDNESS: double
9 TOPOLOGY: linear
10 MOLECULE TYPE: cDNA to mRNA
11 FEATURE:
12 NAME/KEY: CDS
13 LOCATION: 57..1472
14 PRT 1895 07820 1
15
16 Query Match 11.1% Score 40.8; DB 4; Length 1741;
17 Post Local Similarity 48.4%; Pred. No. 0.47;
18 Matches 80; Conserved Yr; 0; Mismatches 84; Indels 0; Gaps 0;
19
20 QY 112 ccccaagcccaatgaatcgaatcaccctaccacacttcacatgaagaaatgctt 171
21 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
22 DB 799 cccagcagcgcgaatgacgagcgcacgacgacgacgacgacgacgacgacgac 858
23 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
24 QY 172 tgaatattgaagacgaatcaagacacaaagagctgaagcaatcaccattatcaacattc 231
25 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
26 DB 859 gacacaaatggcgtatgacacacaaacacgacgacgacgacgacgacgacgacgac 918
27 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
28 QY 232 taccctaccacgaatcaccacgaagcgaagcgaagcgaagcgaagcgaagcgaagc 275
29 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
30 DB 919 tggcgtccctggcgaagcgcgcacgaacgaacgaacgaacgaacgaacgaacgaac 962
31 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
32
33 RESULT 14
34 US-08-689-421-22/c
35 Sequence 22, Application 05/09/9421
36 Patent No. 608029
37
38 GENERAL INFORMATION:
39 APPLICANT: Yaver, Debbie S.
40 APPLICANT: Brown, Kimberly M.
41 APPLICANT: Koppelman, Sakari
42 APPLICANT: Bakker, Torben F.
43 TITLE OF INVENTION: PURIFIED COPOLYMER LACCASES AND NUCLEIC ACIDS
44 TITLE OF INVENTION: ENZYME; SAME
45 NUMBER OF SEQUENCES: 46
46
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE: No. 608029/c No. 608029/c of No. 608029/c of Amer. Inc.
49 STREET: 405 Lexington Avenue, 64th Floor
50 CITY: New York
51 STATE: New York
52 COUNTRY: United States of America
53 ZIP: 10174 6401
54
55 COMPUTER REABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 OPERATING SYSTEM: PC-DOS/MS-DOS
58 SOFTWARE: Patent In Release #1.0, Version #1.80
59
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: 05/09/9421
62 FILING DATE: 9-AUG-1996
63 CLASSIFICATION: 435
64
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Barrington, James J.
67 REGISTRATION NUMBER: 46,711
68 REFERENCE/DOCKET NUMBER: 4554,204-WO
69 TELECOMMUNICATION INFORMATION:
70 TELEPHONE: 212-867 0124
71 TELEFAX: 212-878-9655
72
73 INFORMATION FOR SEQ ID NO: 22:
74 SEQUENCE CHARACTERISTICS:
75 LENGTH: 161 base pairs
76 TYPE: nucleic acid
77 STRANDEDNESS: single

```

[illegible]











Result	No.	Score	Match	%	Query Length	DB	ID	Description
C	1	183.2	66.1	278	2	05-08-454-5276-101	Sequence 101, Appl	
	2	183.2	66.1	278	2	05-08-442-4260-101	Sequence 101, Appl	
	3	183.2	66.1	278	2	05-08-450-6740-101	Sequence 101, Appl	
	4	185.2	66.1	278	4	99T-08595-17111A-101	Sequence 101, Appl	
	5	83.4	12.1	957	3	05-08-126-746-4	Sequence 4, Appl1	
	6	33.4	12.1	1360	5	5225557-3	Patent No. 5225557	
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	8	31.4	11.3	2405	3	05-08-526-146-1	Sequence 1, Appl1	
	9	41.4	11.3	2311	3	05-08-526-146-3	Sequence 4, Appl1	
	10	41.2	11.3	1290	3	05-08-745-977-3	Sequence 3, Appl3	
	11	41.2	11.3	1290	3	05-09-040-609A-4	Sequence 3, Appl1	
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C	13	30.8	11.1	1731	4	99T-08595-07820-1	Sequence 1, Appl1	
	14	30.6	11.0	1161	3	05-08-689-431-22	Sequence 22, Appl1	
	15	30.6	11.0	2004	1	05-08-471-033-18	Sequence 18, Appl1	
	16	30.6	11.0	2004	2	05-08-471-044-18	Sequence 18, Appl1	
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C	19	30.6	11.0	2004	2	05-08-470-566B-18	Sequence 18, Appl1	
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	21	30.6	11.0	2004	3	05-09-300-529-18	Sequence 18, Appl1	
	22	30.6	11.0	2576	1	05-08-471-033-35	Sequence 35, Appl1	
	23	30.6	11.0	2576	2	05-08-471-044-35	Sequence 35, Appl1	
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	30	30.6	11.0	2576	3	05-09-030-529-35	Sequence 35, Appl1	



us-09-490-609b-465.rst

Thu Apr 12 10:22:37 2001









Eukaryotic Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euarchia; Rodentia; Sciurognathi; Muridae; Mus;
(bases 1 to 629)
RFLCAT: L17-2828-ctc1-m-ph-species.asp
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel.: (401) 496-1550 Email: Robert.Strausberg@nih.gov tissue procurement: Gilbert Smith, Ph.D., cDNA library preparation: Life Technologies, Inc., cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINCC) DNA sequencing by: Washington University Genome Sequencing Center clone distribution: NCI CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINCC at: <a href="#">image.html/genemap3/mut/tissues/shiml</a>
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Seq primer: -40BP from Gibco
HIGH QUALITY SEQUENCE SHIP: 436.
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/strain "CZRH 11"
/ <a href="#">ZIL-ZINC:</a> "Taxon:13090"
/ <a href="#">ZIL-ZINC:</a> "IMAGE:4660324"
/ <a href="#">Zilome:</a> "IMAGE:4660324"
/ <a href="#">Zilome_Lib:"NCI_CGAP-Lu30"</a>
/ <a href="#">Zilome_Type:"tumor, metastatic to mammary"</a>
/ <a href="#">Zilome_Host:"BHL0P"</a>
/ <a href="#">Zilome_Organism:"murine"</a> ; Organ: Ventricle; Strain: pMW-SPO976; Site: 1; Not 1; Site_2: Salt; Transgenic model MMTV-L expression driven by MMTV-LTR enhancer; Cloned indirectly; Primer: oligo dT. Library constructed by LIFE technologies. NIH" Invivo: tissue providing samples: Gilbert Smith, NIH"
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Best Local Similarity 91.6%; Pred.No.1:30-56;
Katches 251; Conservative 0; Missmatches 18; Indels 5; gaps 2;
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D6
d6    81   CAACAAMATTGTCGA--GCCACGCTCGAGAGGTCATCTTACACGCCAACPGCTCT 139
QY    124   ataagatcgdtcaaacctaraccaattcacggatgaqaqatgaqtctttaaatcataaa 183
D6
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QY    184   cagaatcatcaadccaagaagatgaqaqatgacaaatfatcaaatctctgaatcaacga 243
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d6    260   GTAAATGTCAGACAGCTAGAGWATTGCTTCGCTCA 293
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AA637875
TITLE
DEFINITION
IMAGE:1122114 y similar to gb:M14043 ANNEXIN II (HUMAN); qb:d10024
Mouse mRNA for protein tyrosine kinase substrate p36 (PRKCE). mRNA sequence.
Accession
AA637875
VERSION
AA637875.1 GI:2561463









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 118: em\_estp17:\*  
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 188: em\_estp87:\*  
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190: qb\_qss25:\*  
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 192: qb\_qss27:\*  
 193: qb\_qss28:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	Hit	Description
1	247	89.2	340	141	H5202	H5202 EST109599.R
2	245	88.4	341	131	HE127203	HE127203 DEPA049
3	242.3	87.5	323	103	AA086091	AA086091 EST109204
4	242	80.1	342	104	HE127664	HE127664 DEPA1413
5	220.8	79.7	606	96	AA010355	AA010355 up80196.Y
6	220.2	79.5	595	1	AA010398	AA010398 md51306.Y
7	219.2	79.1	575	2	AA144415	AA144415 md75a05.Y
8	218	78.7	290	184	HE126540	HE126540 DEPA0288
9	217	78.3	529	139	HE016495	HE016495 up32a07.Y
10	216.6	78.2	584	10	AA037875	AA037875 vt29q10.Y
11	216.2	78.1	608	13	AA069043	AA069043 vt40q10.Y
12	216	78.0	363	87	AA021469	AA021469 up99411.Y
13	215.4	77.8	506	106	HE342710	HE342710 us25105.Y
14	209.6	75.7	724	140	CH0590	CH0590 CH0590.Mous
15	207.8	75.0	400	28	AL364371	AL364371 AL364371
16	207.4	74.9	528	104	HE130087	HE130087 vt34a12.Y
17	205.4	74.2	556	2	AA103617	AA103617 md26107.Y
18	205.4	74.2	667	107	HE37527	HE37527 md1229713
19	205.2	74.1	615	13	AA071247	AA071247 vt42a08.Y
20	205	74.0	388	87	AA021469	AA021469 up99411.Y
21	205	74.0	631	89	AA0321586	AA0321586 up34b12.Y
22	203.6	73.5	667	106	HE306684	HE306684 md1104048
23	201.6	72.8	107	137	HE030527	HE030527 R36.CH0027
24	201.6	72.8	425	108	HE449965	HE449965 HEM1-077F
25	201.2	72.6	656	108	HE449465	HE449465 HEM1-092F
26	201.2	72.6	1118	110	HE573009	HE573009 md1341664
27	200.6	72.4	676	26	AI005511	AI005511 RC-B1091-
28	200.2	72.3	441	186	HE308437	HE308437 md1089957
29	200.2	72.3	548	106	HE409889	HE409889 md1004652
30	200.2	72.2	542	23	AI036454	AI036454 DE32P341E
31	200	72.2	699	26	AI005447	AI005447 RC-B1091-
32	199.8	72.1	910	137	HE004845	HE004845 md1498985
33	199.6	72.1	544	10	AA056250	AA056250 vt12811.Y
34	199.6	72.1	546	147	W09518	W09518 md17811.Y
35	199.6	72.1	652	187	HE469855	HE469855 md1221266
36	199.6	72.1	655	89	AA0321208	AA0321208 md27161.Y
37	199.6	72.1	704	147	W61877	W61877 md16q10.Y
38	199.6	72.1	801	109	HE570179	HE570179 md1341726
39	199.4	72.0	384	38	AV703352	AV703352 AV703352
40	199.4	72.0	517	93	AA071848	AA071848 vt45a04.Y
41	198.9	71.9	427	4	AA148192	AA148192 md01109.Y
42	198.4	71.6	402	5	AA054514	AA054514 NHBR0606
43	198.4	71.6	402	5	AA314924	AA314924 EST186747
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45	198.4	71.6	442	5	AA314318	AA314318 EST186123

ALIGNMENTS

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 DEFINITION EST109599 Rat PC 12 cells, RDE treated (7 days) Ratius Sp. cDNA  
 clone RPNAT19 similar to Annexin II, mRNA sequence.  
 ACCESSION H5202  
 VERSION H5202.1 GI:980619  
 KEYWORDS EST.  
 SOURCE Ratius sp.











































RECEIVED 11  
MAY 1995 04 34 27845  
SEQUENCE 20845, Application US/0054484





Empire Maths	94.69	Score 100	98.17	150015.400
Post Local Similarity	98.29	Prod. No. 4.96.29		
Mathos 103	Conservative	0	Mismatches	27
				Index 17
				Codes 17

RESULT  
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 : Sequence 726, Application 05/09371508  
 : GENERAL INFORMATION  
 : AFFECTANT: GLOCKSMITH, M. Alexander  
 : TITLE: ON INVARIANT, NUCLEIC ACID METABOLITES DERIVED FROM A  
 : FILE REFERENCE: BRAIN LIBRARY  
 : CURRENT ATTENDANT: M. NEMER, 05/05-371, 508  
 : CURRENT FILING DATE: 1999-08-10  
 : EARLIER APPLICATION NUMBER: 652/094, 907  
 : EARLIER FILING DATE: 1998-08-10  
 : EARLIER ATTENDANT: M. NEMER, 05/05-371, 508  
 : EARLIER FILING DATE: 1998-10-05  
 NUMBER OF SEQ. IN NOS: 4611

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 0893-3200/95 \$12.00  
 DOI: 10.1037/0893-3200.10.1.105

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Figure 1:  $\Delta_{\text{eff}} = 1$ ,  $\Delta_{\text{eff}} = 2$ ,  $\Delta_{\text{eff}} = 3$ ,  $\Delta_{\text{eff}} = 4$ ,  $\Delta_{\text{eff}} = 5$ ,  $\Delta_{\text{eff}} = 6$ ,  $\Delta_{\text{eff}} = 7$ ,  $\Delta_{\text{eff}} = 8$ ,  $\Delta_{\text{eff}} = 9$ ,  $\Delta_{\text{eff}} = 10$

127.155, Million of population

[illegible][illegible]

# Scientific Publications

Received: 1994-05-17, revised: 1994-07-16, accepted: 1994-08-01

[illegible][illegible]

For a full discussion of the following material, see the book by (1986).

# THE UNIVERSITY OF CHICAGO

\* VN 540441-10110001 : 02020001001

[illegible]

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proof. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

# SIMPLIFIED

1624

✱

No

20

111

# Introduction

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2	152	91.6	480	17	US-09	471	805	169	Sequence 169, App
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6	141	84.9	553	55	US-09	747	508	726	Sequence 726, App
7	144	74.9	152	20	US-09	551	843	28644	Sequence 28644, App
8	144	74.9	152	17	US-09	471	805	169	Sequence 169, App
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# Acknowledgments

Thu Apr 12 10:22:40 2001

us-09-490-609b-488.rni

Page 10

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[illegible]





INFORMATION FOR STUDENTS:  
SCIENCE CAREERS:



[illegible]



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1 PRESIDENT
2 05/08/4601/298 3/7
3 1. SEQUENCE: 3, Application no. 05/06/0402/08
4 2. Patent No.: 5686,284
5 3. GENERAL INFORMATION:
6 4. APPLICANT: GATTAGY, Thomas D.
7 5. APPLICANT: GATTAGY, Thomas D.
8 6. APPLICANT: LAM, Stephen T.
9 7. APPLICANT: LAM, Stephen T.
10 8. APPLICANT: LLOYD, James M.
11 9. APPLICANT: LITTLE, David S.
12 10. APPLICANT: SOTO, Jeffrey L.
13 11. APPLICANT: HOWELL, Charles R.
14 12. APPLICANT: HOWELL, Charles R.
15 13. APPLICANT: HOWELL, Charles R.
16 14. TITLE OF INVENTION: Gene Amplification Element
17 15. NUMBER OF SEQUENCES: 9
18 16. CORRESPONDENT ADDRESS:
19 17. ADDRESSER: CITICORP Corporation
20 18. STREET: Skyline Drive
21 19. CITY: New York
22 20. STATE: New York
23 21. COUNTRY: USA
24 22. ZIP: 10542
25 23. COMPUTER RELEVABLE FORM:
26 24. MEDIUM TYPE: floppy disk
27 25. COMPUTER: IBM PC compatible
28 26. OPERATING SYSTEM: PC DOS/MS DOS
29 27. SOFTWARE: Follow to Release #1.0, Version #1.25
30 28. CURRENT APPLICATION DATA:
31 29. APPLICATION NUMBER: 05/08/4601/298
32 30. FILING DATE: 02 JUN 1995
33 31. CLASSIFICATION: 5,46
34 32. PRIOR APPLICATION DATA:
35 33. APPLICATION NUMBER: 05/08/297,442
36 34. FILING DATE: 08 AUG 1994
37 35. APPLICATION NUMBER: 05/08/087,646
38 36. FILING DATE: 01 JUL 1994
39 37. PRIOR APPLICATION DATA:
40 38. APPLICATION NUMBER: 05/07/908,284
41 39. FILING DATE: 02 JUL 1992
42 40. PRIOR APPLICATION DATA:
43 41. APPLICATION NUMBER: 05/07/670,184
44 42. FILING DATE: 08 AUG 1990
45 43. ATTORNEY/AGENT INFORMATION:
46 44. NAME: FLORET, James Scott
47 45. REGISTRATION NUMBER: 46,129
48 46. REFERENCE: 2271 PAGES, 527,176,577,4
49 47. TELECOMMUNICATION INFORMATION:
50 48. TELEPHONE: 919 541 8044
51 49. TELEFAX: 919 541 8089
52 50. INFORMATION FOR SEQ ID NO: 4:
53 51. SEQUENCE CHARACTERISTICS:
54 52. LENGTH: 5559 base pairs
55 53. TYPE: nucleic acid
56 54. STRANDEDNESS: single
57 55. TOPOLOGY: linear
58 56. MOLECULE TYPE: DNA (genomic)
59 57. HYPOTHETICAL: No
60 58. ANTI SENSE: No
61 59. ORIGINAL SOURCE:
62 60. ORGANISM: Escherichia Fluorescens
63 61. STRAIN: 676/6/456
64 62. INDIVIDUAL ISOLATE: % 6 kb EcoRI HindIII restriction
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66 64. CLONE: pGEM43
67 65. FEATURE:
68 66. NAME/KEY: misc feature
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71 69. OTHER INFORMATION: "right"
72 70. NAME/KEY: misc feature
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(with all alignments)

149,740 Million cell updates/sec

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us-09-490-609b-488

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Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# RESULTS

Result No.	Score	Gap	Match	Length	DB	ID	Description
1	27.8	16.7	5559	1	US-08-287	442	Sequence 3, Appl 1
2	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
3	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
4	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
5	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
6	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
7	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
8	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
9	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
10	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
11	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
12	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
13	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
14	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
15	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
16	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
17	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
18	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
19	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
20	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
21	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
22	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
23	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
24	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
25	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
26	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
27	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1
28	27.8	16.7	5559	1	US-08-459	701	Sequence 3, Appl 1

29	25.2	15.2	16442	4	US-08-781	891	Sequence 208, Appl 1
30	25.2	15.2	246240	2	US-08-724	904A	Sequence 20, Appl 1
31	25.2	15.2	246240	2	US-08-724	904A	Sequence 21, Appl 1
32	25.2	15.2	246240	2	US-08-724	904A	Sequence 22, Appl 1
33	25.2	15.2	246240	2	US-08-724	904A	Sequence 23, Appl 1
34	25.2	15.2	246240	2	US-08-724	904A	Sequence 24, Appl 1
35	25.2	15.2	246240	2	US-08-724	904A	Sequence 25, Appl 1
36	25.2	15.2	246240	2	US-08-724	904A	Sequence 26, Appl 1
37	25.2	15.2	246240	2	US-08-724	904A	Sequence 27, Appl 1
38	25.2	15.2	246240	2	US-08-724	904A	Sequence 28, Appl 1
39	25.2	15.2	246240	2	US-08-724	904A	Sequence 29, Appl 1
40	25.2	15.2	246240	2	US-08-724	904A	Sequence 30, Appl 1
41	25.2	15.2	246240	2	US-08-724	904A	Sequence 31, Appl 1
42	25.2	15.2	246240	2	US-08-724	904A	Sequence 32, Appl 1
43	25.2	15.2	246240	2	US-08-724	904A	Sequence 33, Appl 1
44	25.2	15.2	246240	2	US-08-724	904A	Sequence 34, Appl 1
45	25.2	15.2	246240	2	US-08-724	904A	Sequence 35, Appl 1

## ALIGNMENTS

RESULT 1  
US-08-287-442 3/c  
Sequence 3, Appl 1  
GENERAL INFORMATION:  
APPLICANT: Galitoy, Thomas D.  
APPLICANT: Lano, Stephen T.  
APPLICANT: Lano, James M.  
APPLICANT: Hill, Dwight S.  
APPLICANT: Stolin, Charles R.  
APPLICANT: Powell, Charles R.  
APPLICANT: Powell, Charles R.  
TITLE OF INVENTION: Group And Leading Element  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10742  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: pc/ios/ms-1008  
SOFTWARE: Patcom to Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/96/267,442  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US-08/2047,636  
FILING DATE: 01-JUL-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US-07/909,284  
FILING DATE: 02-JUL-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US-07/570,184  
FILING DATE: 08-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/KEYWORD: 609 1506/1194  
TELEPHONE: 919-541-8614  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
TYPE: nucleic acid  
LENGTH: 5559 base pairs  
STANDARDNESS: single



PI foodstuffs, and for industrial prodn. of trehalose  
 XX  
 PS Claim 1: Page 118-120; 156pp; English.  
 XX

CC The sequence encodes TSL1 (K41363) and is involved in the expression  
 of TPS (trehalose-6-phosphate synthase) catalytic activities.  
 XX

SU Sequence 5981 BP; 1698 A; 1314 C; 1364 G; 1605 T; 0 other;

Query Match 16.6%; Score 27.6; JH 14; Length 5981;

Best Local Similarity 49.3%; Pred. No. 10;

Matches 69; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 18 ccaagcaataggtctcttcttccatgagcgttcaatctatgacatcgaagtcg 77

Db 1952 cccgcccctgacatttctatataagtgatattgaaattacttgatcaaaatgcttaaatc 2011

QY 78 gttcagctgtccctcagctctcgtcatcgaggaatcgaattcccgaggtttgattga 137

Db 2012 ggtctgaggaagcttgcgcctcgcacgaaggaatagaaagagctggaggtccgagcaac 2071

QY 138 taagcattagcagatgaact 157

Db 2072 gactatgattgacattact 2091

Search completed: April 11, 2001, 19:50:18

Job time: 19011 sec































us-09-490-609b-465.rge

Thu Apr 12 10:22:33 2001

chromosome 9 containing a portion of the T cell receptor beta locus and tyrosinase locus

2 (bases 1 to 216294)

Ward, K., Boyesen, C., Qin, S., Wand, K., Alcorn, M. E., and

Roeder, L. (1997) Department of Molecular Biotechnology, Box

Direct Submission

Submitted (Oct 1997) Department of Molecular Biotechnology, Box

457740 University of Washington, Seattle, Washington 98195, USA

Sequencing technology: high redundancy shotgun, interspersed

repeats were identified with RepeatMasker (available from

http://ftp.cse.washington.edu/RR/RepeatMasker.html). Simple

sequence repeats were identified with SpalnK (available from

http://sourceforge.net/projects/chrtools/chrtools/spalnK.html).

Localizations

1. 216294

Organization: Homo sapiens

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

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chr10:chr10:100000000

(calpain 1 heavy chain) reveals a multidomain protein with

internal repeats

651146 (2), 201-212 (1986)

8624906

A cDNA for the protein-tyrosine kinase substrate, p36 (calpain 1

heavy chain) was cloned and sequenced; the sequence predicts a 339

amino acid protein (molecular weight 44900). The composition

indicates that p36 is rich in charged amino acids (32.2 %). The

sequence homology between p36 and the phosphatase A-2 inhibitor,

lipocortin 1 are found to be about 50 %, suggesting that both are

functionally related; the function of p36 and its kinase are

discussed.

Location/Qualifiers

1. 1107

Organization: Mus musculus

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

chr10:chr10:100000000

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JOURNAL

MECHANISM

COMMENT

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KEYWORDS

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Human Antibodies and Hybridomas ( HUM. ANTIBODIES HYBRIDOMAS ) (United States) 1996, 7/1 (27-36)  
CODEN: HANHE ISSN: 0956-960X  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

...heavy and K light chains. The immunological specificity of the recombinant antibody, was the same as that of hMAb AE6F4 by immunoblotting analysis to the \*14\*-3\*-3\* protein, the putative antigen of hMAb AE6F4, and by immunohistochemical and immunocytological analyses using tissue sections and sputa of lung cancer patients. The transinfected BHK...

\*Lung \*cancer\*--diagnosis\*--di; \*sputum cytodiagnosis

15/3,K/7 (Item 5 from file: 73)

DIALOG(R) File 73:EMBASE  
(c) 2001 Elsevier Science B.V. All rts. reserv.

06433780 EMBASE No: 1996097941

**Immunocytochemical detection of lung cancer cells with monoclonal antibodies to \*14\*-3\*-3\* proteins**

Setoguchi Y.; Kato M.; Shoji M.; Honjo T.; Kamei M.; Sugitani M.; Sato S.; Hashizume S.; Hanagiri T.; Yoshimatsu T.; Nakamishi K.; Yasumoto K.; Nagashima A.; Nakahashi H.; Suzuki T.; Imai T.; Shirahata S.; Nomoto K. Morinaga Inst. of Biological Science, 2-1-1 Shimosueyoshi, Tsurumi-ku, Yokohama 230 Japan

Human Antibodies and Hybridomas ( HUM. ANTIBODIES HYBRIDOMAS ) (United States) 1995, 6/4 (137-144)  
CODEN: HANHE ISSN: 0956-960X  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

**Immunocytochemical detection of lung cancer cells with monoclonal antibodies to \*14\*-3\*-3\* proteins**

Murine monoclonal antibodies were raised against \*14\*-3\*-3\* proteins, the antigen of human monoclonal antibody AE6F4 which had been shown potentially useful for the immunohistochemical diagnosis of lung cancer via sputum cytology. Enzyme-linked immunosorbent assays of the murine anti-\*14\*-3\*-3\* monoclonal antibodies with isolated bovine brain \*14\*-3\*-3\* isoforms showed that the antibodies were classified into four different profiles of isoform reactivity. The comparison of \*14\*-3\*-3\* isoform and lung cancer tissue on the reactivity with murine monoclonal antibodies indicated that beta isoform can be responsible for cancer recognition, whereas human monoclonal...

...was obtained. Since murine monoclonal antibodies with different isoform specificities could immunostain lung cancer cells in sputum successfully, the combination use of murine monoclonal anti-\*14\*-3\*-3\* antibodies with human monoclonal antibody AE6F4 is potentially useful for facilitating the sputum cytodiagnosis of lung cancer.

MEDICAL DESCRIPTORS:

\*Lung \*cancer\*--diagnosis\*--di

15/3,K/8 (Item 6 from file: 73)

DIALOG(R) File 73:EMBASE  
(c) 2001 Elsevier Science B.V. All rts. reserv.

06062667 EMBASE No: 1995093110

**The \*14\*-3\*-3\* protein as the antigen for lung cancer-associated human monoclonal antibody AE6F4**

Shoji M.; Kawamoto S.; Setoguchi Y.; Mochizuki K.; Honjo T.; Kato M.; Hashizume S.; Hanagiri T.; Yoshimatsu T.; Nakamishi K.; Yasumoto K.; Nagashima A.; Nakahashi H.; Suzuki T.; Imai T.; Nomoto K.; Murakami H. Morinaga Inst Biological Science, 2-1-1 Shimosueyoshi, Tsurumi-ku,



... Breast \*Neoplasms\*--DI; Carcinoma--DI; Neoplasms Metastasis

15/3,K/13 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(C) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

134362295 CA: 134(26)362295z PATENT

Endogenous gene expression assay

INVENTOR(AUTHOR): Letters, Henrik; Jorgensen, Marianne; Skakkebaek, Niels Erik

LOCATION: Den.

ASSIGNEE: Rigshospitalet

PATENT: PCT International; WO 0134834 A2 DATE: 20010517

APPLICATION: WO 2000DK628 (20001110) \*DK 991626 (19991111)

PAGES: 76 pp. CODEN: FIXXDE LANGUAGE: English CLASS: C12Q-001/68A

DESIGNATED COUNTRIES: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, FR, GB, GD, GE, GM, GR, HU, ID, IL, IN, IS, JP, KE, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NZ, NO, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TZ, UA, UG, US, VZ, VN, YU, ZA, ZW, AM, AZ, EY, KG, KZ, MD, RU, TJ, TM DESIGNATED REGIONAL: GM, KE, LB, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

15/3,K/14 (Item 2 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(C) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

13439179 CA: 134(24)39179f PATENT

Nucleic acids and proteins associated with cancer as antitumor targets

INVENTOR(AUTHOR): Burmer, Glenna C.; Brown, Joseph P.; Pritchard, David

LOCATION: USA

ASSIGNEE: Lifespan Biosciences, Inc.

PATENT: PCT International; WO 0130964 A2 DATE: 20010503

APPLICATION: WO 2000US29126 (20001020) \*US PVI61232 (19991022)

PAGES: 98 pp. CODEN: FIXXDE LANGUAGE: English CLASS: C12N-000/

CA, CH, CN, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GM, GR, HU, ID, IL, IN, IS, JP, KE, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NZ, NO, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TZ, UA, UG, US, VZ, VN, YU, ZA, ZW, AM, AZ, BY, BG, KZ, MD, RU, TJ, TM DESIGNATED REGIONAL: GM, KE, LB, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

15/3,K/15 (Item 3 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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134235337 CA: 134(17)235337q JOURNAL

Proteomic analysis reveals that 14-3-3.sigma. is down-regulated in human breast cancer cells

AUTHOR(S): Vercauteren-Edouart, Anne-Sophie; Lemoine, Jerome; Le Bourhis, Xuefen; Louis, Hornez; Bolly, Benoit; Nurocombe, Victor; Revillion, Françoise; Peyrat, Jean-Philippe; Hondermarck, Hubert

LOCATION: Equipe Facteurs de Croissance, Laboratoire de Biologie du Développement, UPRES-EA, 1033, Villeneuve d'Ascq, Fr.

JOURNAL: Cancer Res. DATE: 2001 VOLUME: 61 NUMBER: 1 PAGES: 76-80

CODEN: CNREAS ISSN: 0008-5472 LANGUAGE: English PUBLISHER: American Association for Cancer Research



Chemical Name: \*14\*-3\*-3\* protein; Biological Markers; Proteins

15/3,K/10 (Item 2 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

10599731 20270713 PMID: 10810416

Usefulness of urinary nuclear matrix protein 22 (NMP22) as a marker for transitional cell carcinoma of the bladder.

Mendez V; Filieila X; Alcover JA; Molina R; Mallatre JM; Ballesta AM; Talbot-Wright R

Department of Urology, Elche University General Hospital, Miguel Hernandez University, Elche, Spain.

Anticancer research (GREECE) Mar-Apr 2000, 20 (2B) p1169-72, ISSN 0250-7005 Journal Code: 59L

Document type: Journal Article

Record type: Completed

... was 37.8% (17 out of 45), whereas that in post-treatment cases and benign diseases was 30.8% (8 out of 26) compared to \*14\*.3\* (\*3\* out of 21) for healthy volunteers. This cut-off value provided a sensitivity of 37.8% and a specificity of 80.9%. In the bladder...

Descriptors: Bladder \*Neoplasms\*--DI; \*Carcinoma, Transitional Cell--diagnosis--DI; \*Nuclear Proteins--urine--UR; \*Tumor Markers, Biological--urine--UR

15/3,K/11 (Item 3 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

03879151 84230536 PMID: 6547317

A word of caution in the use of neuron-specific enolase expression in tumor diagnosis.

Iranoff G; Bigner DD

Archives of pathology & laboratory medicine (UNITED STATES) Jul 1984, 108 (7) p535, ISSN 0003-9985 Journal Code: 79Z

Contract/Grant No.: 1 P01 CA32672, CA, NCI; 1 P01 NS/CA 20023-01, NS, NINDS; CA11898-13, CA, NCI

Document type: Editorial

Record type: Completed

Descriptors: \*Neoplasms\*--DI; \*Nerve Tissue Proteins; --diagnostic use--DU Chemical Name: \*14\*-3\*-3\* protein; Nerve Tissue Proteins; Phosphorylase Hydrolase

15/3,K/12 (Item 4 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

03757657 81029447 PMID: 6775160

Serum UDP-galactose 4-epimerase as a potential biomarker for breast carcinoma.

Faone JF; Waalkes TP; Baker RR; Shaper JH

Journal of surgical oncology (UNITED STATES) 1980, 15 (1) p59-66, ISSN 0022-4790 Journal Code: K79

Contract/Grant No.: CA06973-16, CA, NCI

Document type: Journal Article

Record type: Completed

... I, II, and III, respectively). Furthermore, when serum GT levels were correlated with the preoperative clinical stage of breast cancer, significant elevations were found in \*14\*.3\* (\*3\*/21) of stage I, 66.7% (8/12) of stage II, 78.6% (11/14) of stage III, and 96.5% (28/29) of stage



Yokohama 230 Japan  
Human Antibodies and Hybridomas ( HUM. ANTIBODIES HYBRIDOMAS ) ( United States ) 1994, 5/3-4 (123-130)  
CODEN: HAHNHE ISSN: 0956-960X  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The \*14\*-3\*-3\* protein as the antigen for lung cancer-associated human monoclonal antibody AE6F4

..AE6F4-derivatized Sepharose 4B column. This 31-kDa protein was identified by the amino acid sequence analysis of the CN Br-cleared fragment as the \*14\*-3\*-3\* family of proteins, the members of which are known to play important physiological roles such as in the regulation of neurotransmitter levels and intracellular signal transduction. The purified \*14\*-3\*-3\* protein from bovine brain showed a comparable M Ab-reacting activity to that of the 31-kDa protein from A549 cells in the enzyme-linked immunosorbent assay (ELISA). The significant reactivity of bovine \*14\*-3\*-3\* protein by MAb AE6F4, shown by the cross inhibition of antibody binding to the coated 31-kDa antigen in ELISA as well as by the inhibition of immunostaining with lung cancer tissues, consistently demonstrated that the antigen(s) recognized by the M Ab was involved in the \*14\*-3\*-3\* protein family. It was found that the expression of the \*14\*-3\*-3\* protein was significantly enhanced in lung cancer tissues compared with the neighbouring normal part of the lung as examined by the immunoblotting method. These results implicated that some member(s) of the \*14\*-3\*-3\* protein family can be the tumor marker(s), providing a rational basis for the immunocytological diagnosis of lung cancer with this human M Ab. MEDICAL DESCRIPTORS: \*cancer\*--\*diagnosis\*--di

15/3,K/9 (Item 1 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

10703171 20411661 PMID: 10953182

\*14\*-3\*-3\* testing in diagnosing Creutzfeldt-Jakob disease: a prospective study in 112 patients.

Lemstra AW; van Meegen MT; Vreijling JP; Meijerink PH; Jansen GH; Bulk S; Baas F; van Gool WA

Department of Neurology, Academic Medical Center, University of Amsterdam, The Netherlands. a.w.lemstra@amc.uva.nl

Neurology (UNITED STATES) Aug 22 2000, 55 (4) p514-6, ISSN 0028-3878 Journal code: N20

Languages: ENGLISH  
Document type: Clinical Trial; Journal Article  
Record type: Completed

\*14\*-3\*-3\* testing in diagnosing Creutzfeldt-Jakob disease: a

prospective study in 112 patients.

OBJECTIVE: To study the sensitivity and specificity of \*14\*-3\*-3\* testing in a prospective series of patients suspected of having Creutzfeldt-Jakob disease (CJD). BACKGROUND: The \*14\*-3\*-3\* protein immunassay on CSF has favorable test characteristics as a pre-mortem diagnostic tool in CJD. However, the \*14\*-3\*-3\* protein is a normal cellular protein expressed in various tissues, and its presence in CSF reflects extensive destruction of brain tissue as in CJD, but also in ischemic stroke and meningoencephalitis. METHODS: \*14\*-3\*-3\* was tested in the CSF of a prospective series of 110 consecutive patients suspected of having CJD. RESULTS: The sensitivity was 97% and the specificity was 87% in this series. False-positive results were mainly caused by stroke and meningoencephalitis. CONCLUSION: The \*14\*-3\*-3\* protein is a highly sensitive and specific marker for CJD when used in the appropriate clinical context.

Descriptors: Astrocytoma--diagnosis--DI; Brain Neoplasms\*--\*diagnosis\*--DI; \*Creutzfeldt-Jakob Syndrome\*--diagnosis--DI; \*Lymphoma\*--diagnosis--DI; \*Proteins--analysis--AN





10774690 EMBASE No: 2000254937

**Simplified labeling approach for synthesizing 3'-deoxy-3'-[sup 1sup]snp**  
**8f]fluorothymidine ([sup 1sup]snp 8f]FLT)**

Machulla H.; Blocher A.; Kuntzsch M.; Piert M.; Wei R.; Grierson J.R.  
H. Machulla, Sektion Radiopharmazie, PET-Zentrum, Universitätsklinikum  
Tübingen, Röntgenweg 15, 72076 Tübingen Germany  
AUTHOR EMAIL: machulla@uni-tuebingen.de  
J. RADIOMAT. NUCL. CHEM. (Hungary) 2000, 243/3 (843-846)  
CODEN: JRNC ISSN: 0236-5731  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH  
NUMBER OF REFERENCES: 5

...In the case of Athy (10 mg), best FLT yields were 5.38+/-1.2 (130  
degreeC, 30 min). Labeling of DMTHy (10 mg) gave \*14\*.3\*% +/- \*3\*.3 at  
[sup 1sup]snp 8f]fluoride the new method allows to produce...  
MEDICAL DESCRIPTORS:  
\*tumor--diagnosis--di; \*cancer\*--\*diagnosis\*--di

15/3,K/5 (Item 3 from file: 73)

DIALOG(R) File 73:EMBASE  
(c) 2001 Elsevier Science B.V. All rts. reserv.

07016576 EMBASE No: 1997307405

**Proteome profiling of bladder squamous cell carcinomas: Identification of  
markers that define their degree of differentiation**

H.; Cells J.E.  
Ostergaard M.; Rasmussen H.H.; Nielsen H.V.; Vorum H.; Orntoft T.F.; Wolf  
J.H. Cells, Department of Medical Biochemistry, Danish Ctr. for Human  
Genome Res., University of Aarhus, Ole Worms Alle, DK-8000 Aarhus C  
Denmark  
Cancer Research ( CANCER RES. ) (United States) 1997, 57/18 (4111-4117)  
CODEN: CNREA ISSN: 0008-5472  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH  
NUMBER OF REFERENCES: 37

...galectin 7 and, in addition, expressed keratins 13, 15, and 19, which  
were not detected in the pure SCC. Involucrin, glutathione S-transferase  
p1, stratifin (\*14\*-3\*-3\* delta), and the SCC antigen 1, on the other  
hand, were less abundant in SCC 589-1. In comparison? less-differentiated  
tumors did not express keratin 10 and were characterized by a decreased  
expression of keratin 14, psoriasin, PA-FABP, galectin 7, and stratifin  
(\*14\*-3\*-3\* ). Indeed, two of these lesions (553-1 and 651-1) could be  
readily lined up in order of decreasing degree of differentiation based on  
the...  
MEDICAL DESCRIPTORS:  
article; \*cancer\* diagnosis; cell differentiation; diagnostic value;  
early diagnosis; human; human tissue; priority journal

15/3,K/6 (Item 4 from file: 73)

DIALOG(R) File 73:EMBASE  
(c) 2001 Elsevier Science B.V. All rts. reserv.

06668352 EMBASE No: 1996333255

**Lung cancer-reacting human recombinant antibody AE6f4: Potential  
usefulness in the sputum cytodiagnosis**

Shoji M.; Kawamoto S.; Seki K.; Teruya K.; Setoguchi Y.; Mochizuki K.;  
Kato M.; Hashizume S.; Hanagiri T.; Yoshimatsu T.; Nakanishi K.; Yasumoto  
K.; Nagashima A.; Nakahashi H.; Suzuki T.; Imai T.; Shitahata S.; Nomoto K.  
Murakami H.  
Morioka Inst. Biological Science, 2-1-1 Shimosueyoshi, Tsurumi-Ku,  
Yokohama 230 Japan



, antibodies to \*14\*-3\*-3\* proteins. The results of the assay demonstrated 7.2 times higher \*14\*-3\*-3\* protein content in the lung cancer tissue (378 + - 200 ng ml-1) as compared with the normal lung (54 + - 35 ng ml-1). These results indicate that the \*14\*-3\*-3\* family of proteins can be an effective marker for lung \*cancer\* \*diagnosis\* such as sputum cytodiagnosis and that \*14\*-3\*-3\* proteins might be involved in the development of lung cancers.

DESCRIPTORS:

CHEMICALS & BIOCHEMICALS: \*14\*-3\*-3\* proteins...

15/3,K/2

(Item 1 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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08628547 Genuine Article#: 309JM No. References: 15

Title: Usefulness of urinary nuclear matrix protein 22 (NMP22) as a marker for transitional cell carcinoma of the bladder

Author(s): Menendez V (REPRINT) ; Filella X; Alcover JA; Molina R; Mallatire JM; Ballesta AM; Talbotwright R

Corporate Source: AVDA ESCANDINAVIA 63 MF7, ALICANTE 03130//SPAIN/

(REPRINT); MIGUEL HERNANDEZ UNIV, EL CHE UNIV, GEN HOSP, DEPT

UROLOG/ELCHE//SPAIN//; HOSP CLIN BARCELONA, IDIBAPS, DEPT CLIN BIOCHEM,

CANC STUDY UNIT/BARCELONA//SPAIN//; HOSP CLIN BARCELONA, DEPT UROL &

RENAL TRANSPLANT/BARCELONA//SPAIN/

Journal: ANTICANCER RESEARCH, 2000, V20, N2B (MAR-APR), P1169-1172

ISSN: 0250-7005 Publication date: 20000300

Publisher: INT INST ANTICANCER RESEARCH, EDITORIAL OFFICE 1ST KM

KAPANDNTIOU-KALAMOU RD KAPANDRITI, POB 22, ATHENS 19014, GREECE

Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

..Abstract: was 37.8% (17 out of 45), whereas that in post-treatment cases and benign diseases was 30.8% (8 out of 26) compared to \*14\*.3\* (\*3\* cut of 21) for healthy volunteers. This cut-off value provided a sensitivity of 37.8% and a specificity of 80.9%. In the bladder...  
..Identifiers--FLOW-CYTOMETRY; FOLLOUP; \*CANCER; \*DIAGNOSIS; \*CYTOLOGY

15/3,K/3

(Item 1 from file: 73)

DIALOG(R) File 73:EMBASE

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11089277 EMBASE No: 2001106912

14-3-3sigma Down-modulation: A ubiquitous marker for breast cancer?

Schmeichel K.

Breast Cancer Research ( United Kingdom ) 2000,

2/5 (373-374)

CODEN: BCRRC ISSN: 1465-5411

DOCUMENT TYPE: Journal ; Note

LANGUAGE: ENGLISH

DRUG DESCRIPTORS:

\*protein \*14\* \*3\* \*3\*--endogenous compound--ec; \*sigma factor--endogenous compound--ec

MEDICAL DESCRIPTORS:

promoter region; methylation; breast carcinogenesis--etiology--et; cancer growth--etiology--et; DNA damage; gene inactivation; breast tumor--etiology

--et; gene silencing; gene control; cancer invasion; \*cancer\* \*diagnosis\*;

human; note

CAS REGISTRY NO.: 136047-16-0 (protein \*14\* \*3\* \*3\*); 9037-42-7 (DNA

methyltransferase); 2353-33-5 (5 aza 2' deoxycytidine)

15/3,K/4

(Item 2 from file: 73)

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S3	347300	NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4	890	CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5	0	(S2 OR S3 OR S4) AND REGUCALCIN
S6	2	(S2 OR S3 OR S4) AND (TSC(W)22)
S7	1	FD (unique items)
S8	18	(S2 OF S3 OF S4) AND (EPOXIDE(W)HYDROLASE)
S9	17	FD (unique items)
S10	5	(S2 OF S3 OF S4) AND BTF
S11	2	FD (unique items)
S12	2	(S2 OF S3 OF S4) AND (ANNEXIN(W)II)
S13	2	FD (unique items)
S14	43	(S2 OF S3 OF S4) AND (14(W)3(W)3)
S15	25	FD (unique items)

MAXKMIC option is not available in file(s): 41, 77, 399

15/3,K/1 (Item 1 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)

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11268954 BIOSIS NO.: 19980050286

Elevated expression levels of the \*14\*-3\*-3\* family of proteins in lung

cancer tissues.

AUTHOR: Nakamishi Kozo(a); Hashizume Shuichi; Kato Masatoshi; Honjo

Tsutsumi; Setoguchi Yuko; Yasumoto Kosei

AUTHOR ADDRESS: (a) Second Dep. Surg., Sch. Med., Univ. Occup. Environ.

Health, 1-1 Iseigaoka, Yahatanishi-ku, Kitakyu Japan

JOURNAL: Human Antibodies 8 (4):p189-194 1997

ISSN: 1093-2607

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

Elevated expression levels of the \*14\*-3\*-3\* family of proteins in lung

cancer tissues.

ABSTRACT: Immunohistochemical staining of lung cancer sections with a murine

monoclonal anti-\*14\*-3\*-3\* antibody showed a sharp discrimination of

the cancer tissue from neighboring normal counterparts in 88 of 121

primary lung cancer tissue specimens of all four...

...of normal and cancerous lung tissue homogenates, each set prepared from

surgically dissected tissues of the cancer and its surrounding normal

part, were assayed for \*14\*-3\*-3\* proteins by the sandwich

enzyme-linked immunosorbent assay using two different monoclonal



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the 'information' and 'communication' fields. The 'information' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information, and the social and cultural contexts in which these activities take place. (p. 1)

The 'communication' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information science' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information studies' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information technology' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information systems' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information science and technology' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information science and communication' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information science and information systems' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

The 'information science and information technology' field is defined as:

...the study of the nature, creation, organisation, storage, retrieval, dissemination and use of information and communication, and the social and cultural contexts in which these activities take place. (p. 1)

proteins. They are also substrates of receptor tyrosine kinases. Overexpression of \*Annexin\* II\*, which has been reported in various carcinomas, is thought to be associated with cell proliferation, differentiation and cell-cell adhesion in the pathogenesis of carcinoma, but the functions of Annexins have not been fully elucidated. In this study, we investigated the role of \*Annexin\* II\* (p36) and its relationship with c-erbB-2 overexpression in gastric carcinoma. We studied \*Annexin\* II\* expression using Western blot analysis in 8 human gastric carcinoma cell lines and expression of \*Annexin\* II\* and c-erbB-2 using immunohistochemistry in 153 primary gastric carcinomas. Western blot revealed that \*Annexin\* II\* was expressed in 8 human gastric carcinoma cell lines. It was more strongly expressed in the cell membrane than in the cytoplasm of tumor cells in primary gastric carcinoma tissues. Thirty-three percent of all cases were immunopositive for \*Annexin\* II\*, overexpression of which was more frequent in differentiated type (p = 0.0009), lymph node, metastasis (p = 0.0147) and venous invasion (p = 0.0092). \*Annexin\* II\* and c-erbB-2 overexpression were significantly correlated p = 0.0002) and patients with \*Annexin\* II\* had poorer prognoses (p = 0.0066). Multivariate analysis showed that immunopositivity of both \*Annexin\* II\* and c-erbB-2 was an independent and poor prognostic factor (p = 0.0037). In conclusion, \*Annexin\* II\* was overexpressed in advanced gastric carcinomas and it could contribute to the progression of gastric carcinoma.

Descriptors: \*Annexin\* II\*--biosynthesis--BI; \*Stomach Neoplasms--metabolism--ME; \*Annexin\* II\*--physiology--PH; Prognosis; Receptor, erbB-2--biosynthesis--BI; \*Stomach Neoplasms\*--\*diagnosis\*--DI; \*Stomach Neoplasms\*--pathology--PA; Tumor Cells, Cultured

Chemical Name: \*Annexin\* II\*; Receptor, erbB-2

13/3,K/2 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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129273909 CA: 129(21)273909g JOURNAL  
Identification of genes expressed differentially by LNCaP or PC-3 prostate cancer cell lines

AUTHOR(S): Yang, Meiheng; Ioda, Massimo; Sytkowski, Arthur J.  
LOCATION: Laboratory for Cell and Molecular Biology, Division of Hematology and Oncology, Department of Medicine, Harvard Medical School, Boston, MA, 02215, USA

JOURNAL: Cancer Res. DATE: 1998 VOLUME: 58 NUMBER: 16 PAGES:

3732-3735 CODEN: CNREA8 ISSN: 0008-5472 LANGUAGE: English PUBLISHER:

3s (s2 or s3 or s4) and ((14(w)3(w)3)

>>>Unmatched parentheses

3s (s2 or s3 or s4) and (14(w)3(w)3)

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890 S4

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17777275 3

6488 14(W)3(W)3

S14 43 (S2 OR S3 OR S4) AND (14(W)3(W)3)

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S15 25 RD (unique items)

show files;ds;t/3,k/all

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Sot Items Description

S1 0 CANCER? WITH (MARKER? OR DIAGNOS?)

S2 97610 CANCER? (W) (MARKER? OR DIAGNOS?)

S3 347300 NEOPLAS? (W) (MARKER? OR DIAGNOS?)

S4 890 CARCINOGEN? (W) (MARKER? OR DIAGNOS?)

S5 0 (S? OR S3 OR S4) AND REGUCALCIN

S6 2 (S? OR S3 OR S4) AND (TSC(W)22)

S7 1 FD (unique items)

S8 18 (S? OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)

S9 17 FD (unique items)

S10 5 (S? OR S3 OR S4) AND BTF

S11 2 FD (unique items)

S12 2 (S? OR S3 OR S4) AND (ANNEXIN(W)II)

S13 2 FD (unique items)

>>>KWIC option is not available in file(s): 41, 77, 399

(13/3,K/1 Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

11488500 21290242 PMID: 11396210

**\*Annexin\* II\* overexpression is correlated with poor prognosis in human gastric carcinoma.**

Emoto K; Sawada H; Yamada Y; Fujimoto H; Takahama Y; Ueno M; Takayama T;

Uchida H; Kamada K; Naito A; Hirao S; Nakajima Y

First Department of Surgery, Nara Medical University, 840 Shijo-cho,

Kashihara, Nara 634-8522, Japan.

Anticancer research (Greece) Mar-Apr 2001, 21 (2B) p1339-45, ISSN

0250-7005 Journal Code: 59L

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

**\*Annexin\* II\* overexpression is correlated with poor prognosis in human gastric carcinoma.**

Annexins belong to a family of the calcium-dependent phospholipid binding

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems.

2. The second section focuses on the role of communication in project management. It highlights the need for clear, concise, and timely communication between team members and stakeholders. The text provides guidelines for effective communication, such as using appropriate channels and formats, and encourages the use of regular meetings and reports to keep everyone informed.

3. The third part of the document addresses the challenges of resource allocation and management. It discusses how to identify and prioritize tasks, allocate resources efficiently, and monitor progress. The text suggests using tools like Gantt charts and PERT diagrams to visualize project timelines and resource usage. It also emphasizes the importance of flexibility in adjusting plans as needed.

4. The final section discusses the importance of risk management. It outlines a process for identifying potential risks, assessing their impact, and developing mitigation strategies. The text stresses that proactive risk management can help prevent problems before they arise and ensure the project stays on track. It also mentions the importance of documenting all risk-related decisions and actions.

97610 S2  
347300 S3  
890 S4  
18158 ANNEXIN  
3840376 II  
2250 ANNEXIN(W)II  
S12 2 (S2 OR S3 OR S4) AND (ANNEXIN(W)II)

2nd  
...completed examining records  
S13 2 PD (unique items)

show files;ds;t/3,r/all

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File 266: FEDRIP 2001/Jul



The International Space Station (ISS) will support several facilities dedicated to scientific research. One such facility, the Biotechnology Facility (\*BTF\*), is sponsored by the Microgravity Sciences and Applications Division (MSAD) and developed at NASA's Johnson Space Center. The \*BTF\* is scheduled for delivery to the ISS via Space Shuttle in April 2005. The purpose of the \*BTF\* is to provide: (1) the support structure and integration capabilities for the individual modules in which biotechnology experiments will be performed, (2) the capability for...

... advances in the understanding of basic and applied biotechnology. Results from planned investigations can be used in applications ranging from rational drug design and testing, \*cancer\* \*diagnosis\* and treatments and tissue engineering leading to replacement tissues.

11/3/K/2 (Item 1 from file: 73)

ILALOG(P) File 73:EMBASE

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10845696 EMBASE No: 2000326389

**Evaluation of two new urinary tumor markers: Bladder tumor fibronectin and cytokeratin 18 for the diagnosis of bladder cancer**

Sanchez-Carbayo M.; Urrutia M.; Gonzalez de Buitrage J.M.; Navajo J.A. M. Sanchez-Carbayo, Laboratorio de Marcadores Tumores, Servicio de Bioquímica, Hospital Universitario de Salamanca, c/Paseo de San Vicente s/n, 37007 Salamanca Spain  
Clinical Cancer Research ( CLIN. CANCER RES. ) (United States) 2000, 6/9  
CODEN: CCREF ISSN: 1078-0432  
(3585-3594)

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH  
NUMBER OF REFERENCES: 53

Our objectives were to evaluate the diagnostic value of two new urinary tumor markers, cytokeratin 18 (CK18) and bladder tumor fibronectin (\*BTF\*), for the detection and monitoring of bladder cancer. The study comprised 931 urine samples belonging to 402 subjects: 112 individuals under suspicion for a primary...

...urological diseases (group 4); and 32 healthy subjects (group 5). Voided urine samples were collected before cystoscopies, between them and before intravesical instillations. CK18 and \*BTF\* tests were measured by chemiluminescent immunoassays. Optimal receiver operating characteristic cutoffs of 7.4 mug/L for CK18 and 52.8 mug/liter for \*BTF\* rendered overall sensitivities of 66.2% for CK18 and 80.0% for \*BTF\* at specificities of 89.4 and 74.7%, respectively. Urinary cytology provided a sensitivity of 29.2% at a specificity of 99.1%. Sensitivities were 80.8, 74.2, and 82.3% for \*BTF\* and 71.1, 77.4, and 64.7% for CK18 for groups 1 to 3, respectively. False positive rates were higher for \*BTF\* in all groups of patients. Elevated urinary tumor markers during the monitoring of patients with bladder cancer could detect recurrence sooner than scheduled cystoscopies. Persistence of negative markers was greatly indicative of free of disease status in follow-up. CK18 and \*BTF\* in urine may eventually prove to be of benefit for specific patients with bladder carcinoma given its higher sensitivity compared with cytology. In selected patients, namely those with persistent negative urinary CK18 and \*BTF\*, the number of cystoscopies could be reduced.

MEDICAL DESCRIPTORS:

\*bladder \*cancer\*--\*diagnosis\*--di

\*cancer\* \*diagnosis\* ; \*diagnostic value\* ; cystoscopy ; chemoluminescence ; immunoassay ; receiver operating characteristic ; urine cytology ; diagnostic accuracy ; cancer recurrence ; human ; male ; female ; major clinical study ; controlled study ; human cell ; aged...

75 (s2 or s3 or s4) and (annexin(w)ii)



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Set	Items	Description
S1	0	CANCER? WITH (MARKER? OR DIAGNOS?)
S2	97610	CANCER? (W) (MARKER? OR DIAGNOS?)
S3	347300	NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4	890	CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5	0	(S2 OR S3 OR S4) AND REGUCALCIN
S6	2	(S2 OR S3 OR S4) AND (TSC(W)22)
S7	1	RD (unique items)
S8	18	(S2 OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)
S9	17	RD (unique items)
S10	5	(S2 OR S3 OR S4) AND BTF
S11	2	RD (unique items)

>>>KWIC option is not available in file(s): 41, 77, 399

11/3,K/1 (Item 1 from file: 6)

DIALOG(R)File 6:NTIS

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2186676 NTIS Accession Number: N20000112941/XAB

**Biotechnology Facility: An ISS Microgravity Research Facility**

Gonda, S. R.; Tsao, Y. M.

National Aeronautics and Space Administration, Houston, TX, Lyndon B. Johnson Space Center.

Corp. Source Codes: 019042004; ND185000

Report No.: AIAA PAPER 2000-0430

2000 9p

Languages: English

Journal Announcement: USGRLR0105; STAR3967

Presented at Aerospace Sciences 38th Reno, NV 10-13 Jan. 2000. American

Inst. of Aeronautics and Astronautics, Reston, VA.

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DESCRIPORS: rat cytosol low abundance \*epoxide\*-hydrolyase\*, gene cloning, polymerase chain reaction, pot. \*cancer\* \*diagnosis\* enzyme EC-3.3.2.2

tumor (Vol.12, No.21)  
?s (s2 or s3 or s4) and btf

97610 S2  
347300 S3  
890 S4  
566 BTF  
S10 5 (s2 OR S3 OR S4) AND BTF

2nd

...completed examining records

S11 2 RD (unique items)

show files;ds/t/3,k/all

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9/3,K/15 (Item 2 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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100083582 CA: 100(11) 83582Z JOURNAL  
Epoxide hydrolase: a marker for experimental hepatocarcinogenesis

AUTHOR(S): Giffin, Martin J.; Gengozian, Nazareth  
LOCATION: Cancer Res. Program, Oklahoma Med. Res. Found., Oklahoma City,  
OK, 73104, USA  
JOURNAL: Ann. Clin. Lab. Sci. DATE: 1984 VOLUME: 14 NUMBER: 1 PAGES:  
27-31 CODEN: ACLSCP ISSN: 0091-7370 LANGUAGE: English

9/3,K/16 (Item 1 from file: 266)

DIALOG(R) File 266:FEDRIP

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00307010

IDENTIFYING NO.: 5R01ES05116-10 AGENCY CODE: CRISP

BIOLOGICAL MARKERS OF AFLATOXIN EXPOSURE

PRINCIPAL INVESTIGATOR: SANTELLA, REGINA M  
ADDRESS: COLUMBIA UNIVERSITY 701 W 168TH ST NEW YORK, NY 10032  
PERFORMING ORG.: COLUMBIA UNIVERSITY HEALTH SCIENCES, NEW YORK  
SPONSORING ORG.: NATIONAL INSTITUTE OF ENVIRONMENTAL HEALTH SCIENCES  
FY : 2001

...SUMMARY: of carcinogens are partly responsible for inter-individual  
differences in AFB1 adduct levels, by determination of genotype for  
glutathione S-transferase M1 and T1, and \*epoxide\*hydrolase\*. Since  
genotyping methods are currently unavailable to examine the role of  
polymorphisms in cytochrome P450 3A4 and 1A2, a quantitative  
immunohistochemical technique for phenotyping will...  
DESCRIPTORS: biomarker; blood chemistry; urinalysis; genotype; Taiwan;  
human subject; \*epoxide\*hydrolase\*; immunocytochemistry; western blotting  
; hepatitis B antigen; environment related neoplasm/cancer; nutrition  
aspect of cancer; neoplasm/\*cancer\*diagnosis\*; hepatocellular carcinoma;  
cancer risk; nutrition related tag; toxicant interaction; Asian; aflatoxin;  
toxin metabolism; glutathione transferase; DNA damage; enzyme activity;  
oxidative stress; smoking; clinical research

9/3,K/17

(Item 1 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs

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0154125 DBA Accession No.: 93-12177

The use of the PCR technique in cloning low abundant genes: isolation of a  
cytosolic \*epoxide\*hydrolase\* cDNA- enzyme isolation, purification  
and gene cloning by the polymerase chain reaction; potential \*cancer\*  
\*diagnosis\* (conference paper)

AUTHOR: Knehr M; Arand M; Hagen M; Zeller H D; Thomas H; Gsch F  
CORPORATE SOURCE: Institute of Toxicology, University of Mainz, Obere  
Zahlbacherstr. 67, D-6500 Mainz, Germany.

JOURNAL: Eur.Biotechnol.Today (217-22) 1992

CODEN: 9999S

LANGUAGE: English

The use of the PCR technique in cloning low abundant genes: isolation of a  
cytosolic \*epoxide\*hydrolase\* cDNA- enzyme isolation, purification  
and gene cloning by the polymerase chain reaction; potential \*cancer\*  
\*diagnosis\* (conference paper)

ABSTRACT: Cytosolic \*epoxide\*hydrolase\* (CEH, EC-3.3.2.2) was isolated  
and purified from a tiadenol-induced male rat cytosol and peptide  
fragments were generated by endoprotease Glu...

the first of these is the fact that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The second is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The third is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

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The first of these is the fact that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The second is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The third is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The first of these is the fact that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The second is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The third is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

RESPIRATORY TRACT DISEASES--Physiopathology--PF; MOUTH DISEASES--Pathology  
--PA; TOOTH DISEASES--Pathology--PA; SUBSTANCE-RELATED DISORDERS; POISONING  
; ANIMALS, LABORATORY; DIAGNOSIS; \*NEOPLASMS\*--DI; \*NEOPLASMS  
--Pathology--PA; NEOPLASMS--Metabolism--ME; MORBIDITY; NEOPLASMS; HOMINIDAE

9/3,K/12 (Item 3 from file: 156)

DIALOG(R) File 156:Toxline(R)

(C) format only 2000 The Dialog Corporation. All rts. reserv.

03071639 Subfile: BIOSIS-91-13126

Cytochrome P-450 isozyme pattern is related to individual susceptibility  
to diethylnitrosamine-induced liver cancer in rats.

AITIO A; AITIO M-L; CAMUS A-M; CARDIS E; BARTSCH H

Lab. Biochem., Inst. Occup. Health, Arinatie 3, 00370 Helsinki, Finl.

Source: JPN J CANCER RES; 82 (2). 1991. 146-156. Coden: JJCRC

Language: ENGLISH

BIOSIS COPYRIGHT: BIOL ABS.

... of the latency period of hepatocellular tumors in individual rats was  
negatively related to the activities of hepatic dimethylnitrosamine  
N-demethylase, aryl hydrocarbon hydroxylase and \*epoxide\* \*hydroxylase\* and  
positively related to the amount of microsomal protein. Consistent  
relationships between the other 10 measured parameters and the  
susceptibility to DEN-induced carcinogenesis were...

Descriptors/keywords: ...; AMINO ACIDS; PEPTIDES; PROTEINS; COENZYMES;  
ENZYMES; ENZYMES--Analysis--AN; ENZYMES--Physiology--PH; DIGESTIVE SYSTEM  
DISEASES--Pathology--PA; DIGESTIVE SYSTEM--Pathology--PA; POISONING;  
ANIMALS, LABORATORY; DIAGNOSIS; \*NEOPLASMS\*--DI; MURIDAE

9/3,K/13 (Item 4 from file: 156)

DIALOG(R) File 156:Toxline(R)

(C) format only 2000 The Dialog Corporation. All rts. reserv.

02938869 Subfile: BIOSIS-87-24413

DETECTION OF PRENEOPLASTIC LIVER LESIONS IN THE RAT BY USE OF MONOCLONAL  
ANTIBODIES AGAINST MICROSOMAL \*EPOXIDE\* \*HYDROLASE\*

Source: FOURTH SYMPOSIUM OF THE DEUTSCHEN KREBSGESELLSCHAFT, SECTION OF  
BRAUNLING O; BUCHMANN A; PESCHKE P; BURGER R; OESCH E; SCHWARZ M; KUNZ W

EXPERIMENTELLE KREBSFORSCHUNG (GERMAN CANCER SOCIETY, SECTION OF  
EXPERIMENTAL CANCER RESEARCH), HEIDELBERG, WEST GERMANY, MARCH 18-21, 1987.

Language: ENGLISH

BIOSIS COPYRIGHT: BIOL ABS. RRM

DETECTION OF PRENEOPLASTIC LIVER LESIONS IN THE RAT BY USE OF MONOCLONAL  
ANTIBODIES AGAINST MICROSOMAL \*EPOXIDE\* \*HYDROLASE\*  
Descriptors/keywords: CONGRESSES; BIOLOGY; BIOCHEMISTRY; AMINO ACIDS;  
PEPTIDES; PROTEINS; CARBOHYDRATES; ENZYMES--Physiology--PH; DIGESTIVE  
SYSTEM DISEASES--Pathology--PA; DIGESTIVE SYSTEM--Pathology--PA; DIAGNOSIS;  
\*NEOPLASMS\*--DI; IMMUNITY; IMMUNOCHEMISTRY--Instrumentation  
--IS; IMMUNOCHEMISTRY--Methods--MT; MURIDAE

9/3,K/14 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(C) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

104144641 CA: 104(17)144641Y PATENT

Monitoring preneoplastic antigen

INVENTOR(AUTHOR): Hammock, Bruce D.; Ota, Kenji

LOCATION: USA

ASSIGNEE: University of California, Berkeley

PATENT: United States ; US 4558004 A DATE: 851210

APPLICATION: US 478962 (830325)

PAGES: 3 pp. CODEN: USXXAM LANGUAGE: English CLASS: 435004000;





they were not even asked for a blood specimen until at least several years after their initial interview, and at that... to assess association with lung cancer susceptibility. Carcinogenesis 1991;12:1533-7.

19. Heckbert SR, Weiss NS, Hornung SK, et al. Glutathione S-transferase and \*epoxide\* \*hydrolase\* activity in human leukocytes in relation to risk of lung cancer and other smoking-related cancers. J Natl Cancer Inst 1992;84:414-22.

20...

9/3,K/10 (Item 1 from file: 156)

DIALOG(R)File 156:Toxline(R)

(c) format only 2000 The Dialog Corporation. All rts. reserv.

03606586 Subfile: CRISP-99-ES05116-08

BIOLOGICAL MARKERS OF AFLATOXIN EXPOSURE

SANTELLA RM

COLUMBIA UNIVERSITY, 701 WEST 168TH STR, HHSC 5-506, NEW YORK, NY 10032  
Source: Crisp Data Base National Institutes of Health

Language: ENGLISH

Document Type: Research

Spon. Agency: U.S. DEPT. OF HEALTH AND HUMAN SERVICES; PUBLIC HEALTH SERVICE; NATIONAL INST. OF HEALTH, NATIONAL INSTITUTE OF ENVIRONMENTAL HEALTH SCIENCES

Contract Number: 5R01ES05116-08

Award Type: Grant

...of carcinogens are partly responsible for inter-individual differences in AFB1 adduct levels, by determination of genotype for glutathione S-transferase M1 and T1, and \*epoxide\* \*hydrolase\* . Since genotyping methods are currently unavailable to examine the role of polymorphisms in cytochrome P450 3A4 and 1A2, a quantitative immunohistochemical technique for phenotyping will...

Descriptors/Keywords: biomarker; blood chemistry; urinalysis; genotype; Taiwan; human subject; \*epoxide\* \*hydrolase\*; immunocytochemistry; western blotting; hepatitis B antigen; environment related neoplasm /cancer; nutrition aspect of cancer; neoplasm /cancer\* \*diagnosis\*; hepatocellular carcinoma; cancer risk; nutrition related tag; toxicant interaction; Asian /Pacific Islander; aflatoxin; toxin metabolism; glutathione transferase; DNA damage; enzyme activity; oxidative stress; smoking; clinical...

9/3,K/11 (Item 2 from file: 156)

DIALOG(R)File 156:Toxline(R)

(c) format only 2000 The Dialog Corporation. All rts. reserv.

03125275 Subfile: BIOSIS-92-29499

Glutathione S-transferase and \*epoxide\* \*hydrolase\* activity in human leukocytes in relation to risk of lung cancer and other smoking-related cancers.

HECKBERT SR; WEISS NS; HORNUNG SK; EATON DL; MOTULSKY AG

Dep. Epidemiol. SC-36, Univ. Washington, Seattle, Wash. 98195.

Source: J NATL CANCER INST (BETHESDA); 84 (6). 1992. 414-422. Coden: JNCIE

Language: ENGLISH

BIOSIS COPYRIGHT: BIOL ABS.

Glutathione S-transferase and \*epoxide\* \*hydrolase\* activity in human leukocytes in relation to risk of lung cancer and other smoking-related cancers.

... based, case-control study to determine whether patients with cancers related to smoking had lower activity of detoxifying isoenzymes of glutathione S-transferase (GST) and \*epoxide\* \*hydrolase\* (EH) than control subjects. Enzyme activities were measured in leukocytes from 113 King County (Washington) residents diagnosed during 1987 with one of three smoking-related...  
Descriptors/Keywords: ...; PA; UROLOGIC DISEASES--Physiopathology--PP;

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glutathione transferase)

9/3,K/8 (Item 5 from file: 73)

DIALOG(R) File 73:EMBASE

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05332142 EMBASE No: 1993100227

**Expression of xenobiotic metabolizing enzymes in breast cancer**

Murray G.I.; Weaver R.J.; Paterson P.J.; Ewen S.W.B.; Melvin W.T.; Burke M.D.

Department of Pathology, University of Aberdeen, Foresterhill, Aberdeen

AB9 22D United Kingdom

Journal of Pathology ( J. PATHOL. ) (United Kingdom) 1993, 169/3

(347-353)

CODEN: JPTLA ISSN: 0022-3417

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

...the expression of different xenobiotic metabolizing enzymes in primary operable breast cancer of no special type. The expression of two forms of cytochrome P450, microsomal \*epoxide\* \*hydroxylase\*, and three classes of glutathione S-transferase was investigated using immunohistochemistry. The tumours were characterized by consistent expression of microsomal \*epoxide\* \*hydroxylase\* and by variable expression of the two forms of cytochrome P450 and the three types of glutathione S-transferase. Cytochrome P450 1A and cytochrome P450 3A were identified in 39 and 22 per cent of tumours, respectively. In each case, immunostaining was present only in areas of invasive carcinoma. \*Epoxide\* \*hydroxylase\* was identified in 89 per cent of tumours and glutathione S-transferases pi, mu, and alpha were identified in 56, 65, and 44 per cent of tumours, respectively. Immunoreactivity for \*epoxide\* \*hydroxylase\* and glutathione S-transferases was identified in both tumours and non-neoplastic breast tissue. The presence of different xenobiotic metabolizing enzymes may have a role...

DRUG DESCRIPTIONS:  
\*cytochrome p450--endogenous compound--ec; \*epoxide\* \*hydroxylase\*  
--endogenous compound--ec; \*glutathione transferase--endogenous compound  
--ec  
MEDICAL DESCRIPTIONS:  
\*breast \*cancer\*--diagnosis\*--di  
...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* \*hydroxylase\*); 50812-37-8 ( glutathione transferase)

9/3,K/9

(Item 1 from file: 98)

DIALOG(R) File 98:General Sci Abs/Full-Text

(c) 2001 The HW Wilson Co. All rts. reserv.

04054096 H.W. WILSON RECORD NUMBER: BGSA99054096 (USE FORMAT 7 FOR

FullText)

**Glutathione S-Transferase M1 genotypes and the risk of squamous carcinoma**

**of the cervix: a population-based case-control study.**

Chen, Chu

Madeleine, Margaret M; Weiss, Noel S

American Journal of Epidemiology (Am J Epidemiol) v. 150 no6 (Sept. 15

1999) p. 569-72

SPECIAL FEATURES: bibl 11 ISSN: 0002-9262

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 2881

(USE FORMAT 7 FOR FullText)

TEXT:

... several limitations. First, blood samples for genotyping were not obtained on all potentially eligible study subjects. This was a particular problem for women with cervical \*cancer\* \*diagnosed\* in the 1980s, since

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the information.

2. The second section focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication, both internally and externally. The text provides examples of effective communication strategies, such as regular meetings, newsletters, and open-door policies. It also discusses the challenges of communication, such as language barriers and cultural differences, and offers suggestions for overcoming these obstacles.

3. The third part of the document addresses the issue of resource management. It discusses the importance of identifying and allocating resources effectively to support the organization's mission. The text provides a framework for assessing resource needs and developing a plan to meet them. It also mentions the importance of monitoring and evaluating resource usage to ensure that resources are being used efficiently and effectively.

4. The final section of the document discusses the importance of continuous improvement. It emphasizes that organizations should be constantly seeking ways to improve their processes and performance. The text provides a framework for identifying areas for improvement and implementing changes. It also mentions the importance of involving employees in the improvement process, as they are often the best source of ideas and feedback.

...lung tissues in 12 patients. The following enzymes were assayed by Western blot analysis: cytochromes P-450 (1A1/A2, 2B1/B2, 2C8-10, 2E1, 3A4); \*epoxide\* and glutathione S-transferase isoenzymes (GST-alpha, -mu, and -pi). The activity of the following enzymes or cofactor were determined by spectrophotometric or fluorometric assays...

...GST activity and GST-alpha or GST-pi. No significant difference was observed for the glucuronide and the sulfate pathways and their corresponding hydrolytic enzymes. \*Epoxide\* and \*hydroxylase\* was significantly decreased in tumors compared to nontumoral lung tissues ( $P < 0.05$ ). In conclusion, these results showed differences between non-small cell lung tumors and nontumoral tissues for cytochrome P-450 1A1/A2 and \*epoxide\* and \*hydroxylase\*. These differences between tumors and peritumoral tissues with regard to these drug-metabolizing enzymes could reflect differences occurring after malignant transformation and may play a...

DRUG DESCRIPTIONS: \*beta glucuronidase--endogenous compound--ec; cytochrome P450--endogenous compound--ec; \*epoxide\* and \*hydroxylase\*--endogenous compound--ec; \*glucuronosyltransferase--endogenous compound--ec; \*glutathione--endogenous compound--ec; \*sulfatase--endogenous compound--ec; \*sulfotransferase--endogenous compound--ec

MEDICAL DESCRIPTIONS: \*lung non small cell cancer--surgery--su; \*lung non small cell cancer--diagnosis--di; \*lung parenchyma

...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* and \*hydroxylase\*); 37329-64-9...

9/3,K/7 (item 4 from file: 73)

DIALOG(R) file 73:EMBASE

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05506462 EMBASE No: 1993274561

**Xenobiotic metabolizing enzyme expression in colonic neoplasia**

McKay J.A.; Murray G.I.; Weaver R.J.; Ewen S.W.B.; Melvin W.T.; Burke

M.D.

Department of Pathology, University of Aberdeen, Foresterhill, Aberdeen

AB9 2ZD United Kingdom

Gut (GUT) (United Kingdom) 1993, 34/9 (1234-1239)

CODEN: GUTTA ISSN: 0017-5749

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The cytochrome P450, \*epoxide\* and \*hydroxylase\*, and glutathione S-transferase enzyme families play an important part in the metabolism of many carcinogens and anti-cancer drugs. The expression of two forms of cytochrome P450 (P450 1A and P450 3A), \*epoxide\* and \*hydroxylase\* and of the alpha, mu, and pi forms of glutathione S-transferase in normal colonic adenomas, and adenocarcinoma of the colon were studied by...

...glutathione S-transferase pi was also present in chronic inflammatory cells. Cytochrome P450 was present in only a small proportion of normal colon samples, whereas \*epoxide\* and \*hydroxylase\* and glutathione S-transferase mu were identified in about half, and glutathione S-transferase alpha and pi in most normal samples. By contrast all the...

...and in over half the carcinomas. These results suggest that cytochrome P450 1A and cytochrome P450 3A are more specific markers of colonic neoplasia than \*epoxide\* and \*hydroxylase\* or glutathione S-transferases alpha, mu, and pi.

DRUG DESCRIPTIONS: \*enzyme; \*tumor marker; \*antineoplastic agent--pharmacokinetics--pk; \*cytochrome P450--endogenous compound--ec; \*epoxide\* and \*hydroxylase\*--endogenous compound--ec; \*glutathione transferase--endogenous compound--ec

MEDICAL DESCRIPTIONS:

\*colon cancer--diagnosis--di; \*drug metabolism; \*xenobiotic metabolism

...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* and \*hydroxylase\*); 50812-37-8 (

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... published results for Caucasians are somewhat variable, the association among African-Americans in these data provides some support for the hypothesis that genetically reduced microsomal \*epoxide\* \*hydroxylase\* activity may be protective against lung cancer. (C) 2000 Elsevier Science Ireland Ltd.  
DRUG DESCRIPTORS:  
\*epoxide\* \*hydroxylase\*--endogenous compound--ec; \*benzo[a]pyrene--drug toxicity--to; \*tobacco--drug toxicity--to  
MEDICAL DESCRIPTORS:  
\*smoking; \*lung \*cancer\*--diagnosis\*--di; \*lung cancer--etiology--et; \*cancer risk  
...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* \*hydroxylase\*); 50-32-8 (benzo[a]pyrene)

9/3,K/5 (Item 2 from file: 73)

DIALOG(R) file 73:EMBASE  
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EMBASE No: 1999126632

**Genetic polymorphism of xenobiotic metabolizing enzymes among Chinese lung cancer patients**

Persson I.; Johansson I.; Lou Y.-C.; Yue Q.-Y.; Duan L.-S.; Bertilsson L.; Ingelman-Sundberg M.

I. Persson, Institute of Environmental Medicine, Division of Molecular Toxicology, Karolinska Institutet, 171 77 Stockholm Sweden  
AUTHOR EMAIL: irene.persson@tm.ki.se

International Journal of Cancer (INT. J. CANCER) (United States) 1999  
81/3 (325-329)  
CODEN: IJCA ISSN: 0020-7136

DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 19

...cancer susceptibility. Several studies have indicated an association between variant alleles of the human CYP1A1, CYP2E1 and GSTM1 genes and lung cancer. Activity of microsomal \*epoxide\* \*hydroxylase\* (HXL) has also been associated with lung cancer, and 2 variant alleles causing amino acid substitutions have been described. We have investigated genetic polymorphisms of...  
MEDICAL DESCRIPTORS:  
\*lung \*cancer\*--diagnosis\*--di; \*lung cancer--epidemiology--ep; \*lung cancer--etiology--et; \*genetic polymorphism; \*xenobiotic metabolism; \*ethnic difference

9/3,K/6 (Item 3 from file: 73)

DIALOG(R) file 73:EMBASE  
(C) 2001 Elsevier Science B.V. All rts. reserv.

EMBASE No: 1993304401

**Main drug- and carcinogen-metabolizing enzyme systems in human non-small cell lung cancer and peritumoral tissues**

Toussaint C.; Albin N.; Massaad L.; Grunewald D.; Parise Jr. O.; Morizet J.; Gouyette A.; Chabot G.G.

Institut Gustave-Roussy, Pavillon de recherche 2, 94805 Villejuif Cedex France  
Cancer Research ( CANCER RES. ) (United States) 1993, 53/18 (4608-4612)  
CODEN: CNREA ISSN: 0008-5472

DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH





02079661 Genuine Article#: J2430 No. References: 55

**Title: COMPARISON OF MOUSE AND HUMAN COLON TUMORS WITH REGARD TO PHASE-I AND PHASE-II DRUG-METABOLIZING ENZYME-SYSTEMS**

Author(s): MASSAAD L; DEWAZIERS I; RIBRAG V; JANOT F; BEAUNE PH; MORIZET J; GOUETTE A; CHABOT G

Corporate Source: INST GUSTAVE ROUSSY, PHARMACOL CLIN

LAB, CNRS, URA147, INSERM, U140/F-94805 VILLEJUIF//FRANCE//; CHU NECKER

ENFANTS MALAD, INSERM LAB, U75/F-75730 PARIS 15//FRANCE//

Journal: CANCER RESEARCH, 1992, V52, N23 (DEC 1), P6567-6575

ISSN: 0008-5472

Language: ENGLISH Document Type: ARTICLE (Abstract Available)

...Abstract: both tumoral and nontumoral colon tissues. The following enzymes were assayed by Western blot: cytochromes P-450 (1A1/A2, 2B1/B2, 2C, 2E1, and 3A), \*epoxide\* \*hydrolase\*, and glutathione-S-transferases (GST- $\alpha$ , - $\mu$ , and - $\pi$ ). The activities of the following enzymes or cofactors were determined by spectrophotometric or fluorometric assays: total cytochrome P-450, 1-chloro-2,4-dinitrobenzene-GST, selenium-independent glutathione peroxidase, 3,4-dichloronitrobenzene-GST, ethacrynic acid-GST, total glutathione, \*epoxide\* \*hydrolase\*, UDP-glucuronosyltransferase, beta-glucuronidase, sulfoltransferase, and sulfatase. Results obtained by Western blot showed that mouse colon adenocarcinoma Co38 did not express any of the probed...

...fold higher in human tumors than in peritumoral tissues, whereas they were 7-fold lower in mouse colon tumor Co38, compared to normal mouse colon. \*Epoxide\* \*hydrolase\* was not expressed in either mouse colon adenocarcinoma Co38 or normal mouse colon tissues, whereas it was expressed in human colon peritumoral and tumoral tissues...

...Identifiers--GLUTATHIONE-S-TRANSFERASE; HUMAN-LIVER; AROMATIC-HYDROCARBONS; MULTIDRUG RESISTANCE; HUMAN-TISSUES; RAT-LIVER; CYTOCHROME-P-450; PURIFICATION; \*CANCER\*; \*MARKER\*

9/3,K/4 (Item 1 from file: 73)

DIALOG(F) File 73:EMBASE

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10626265 EMBASE No: 2000092044

**Lung cancer risk in relation to genetic polymorphisms of microsomal \*epoxide\* \*hydrolase\* among African-Americans and Caucasians in Los Angeles County**

London S.J.; Smart J.; Daly A.K.

S.J. London, Epidemiology Branch, Natl. Inst. of Environ. Health Sci., PO Box 12233, Research Triangle Park, NC 27709 United States

AUTHOR EMAIL: london2@niehs.nih.gov

Lung Cancer ( LUNG CANCER ) (Ireland) 2000, 28/2 (147-155)

CODEN: LUCAE ISSN: 0169-5002

PUBLISHER ITEM IDENTIFIER: S0169500299001300

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 15

**Lung cancer risk in relation to genetic polymorphisms of microsomal \*epoxide\* \*hydrolase\* among African-Americans and Caucasians in Los Angeles County**

...08, 95. CI 0.01-0.62). When data from both the exon 3 and exon 4

[Faint, illegible text covering the majority of the page, likely bleed-through from the reverse side.]

Set Items Description

SI	Items	Description
S1	0	CANCER? WITH (MARKER? OR DIAGNOS?)
S2	97610	CANCER? (W) (MARKER? OR DIAGNOS?)
S3	347300	NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4	890	CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5	0	(S2 OR S3 OR S4) AND REGUCALCIN
S6	2	(S2 OR S3 OR S4) AND (TSC(W)22)
S7	1	RD (unique items)
S8	18	(S2 OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)
S9	17	RD (unique items)

>>>KWIC option is not available in file(s): 41, 77, 399

9/3,K/1 (Item 1 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)  
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05370628 BIOSIS NO.: 000032093757

**IMMUNOCHEMICAL DETERMINATION OF MICROSOMAL \*EPOXIDE\* \*HYDROLASE\***  
**PRENEOPLASTIC ANTIGEN IN EXTRAHEPATIC TISSUE**

AUTHOR: MOODY D E; LOURY D N; HAMMOCK B D  
AUTHOR ADDRESS: CENT. FOR HUMAN TOXICOL., 38 SKAGGS HALL, UNIV. OF UTAH,  
SALT LAKE CITY, UTAH 84112.

JOURNAL: BIOCHEM PHARMACOL 36 (4). 1987. 570-572. 1987  
FULL JOURNAL NAME: Biochemical Pharmacology

CODEN: BOPCA  
RECORD TYPE: citation  
LANGUAGE: ENGLISH

**IMMUNOCHEMICAL DETERMINATION OF MICROSOMAL \*EPOXIDE\* \*HYDROLASE\***  
**PRENEOPLASTIC ANTIGEN IN EXTRAHEPATIC TISSUE**  
DESCRIPTORS: RAT DIAGNOSIS \*NEOPLASTIC\* MARKER\* CARCINOGENESIS

9/3,K/2 (Item 1 from file: 34)

DIALOG(R) File 34: SciSearch(R) cited Ref Sci  
(c) 2001 Inst for Sci Info. All rts. reserv.

05970832 Genuine Article#: XLI62 No. References: 49

**Title: Tumor-specific expression of cytochrome P450 CYP1B1**

Author(s): Murray GI (REPRINT); Taylor MC; McFadyen MCE; McKay JA;  
Greenlee WF; Burke MD; Melvin WT

Corporate Source: UNIV ABERDEEN, DEPT PATHOL, FORESTERHILL/ABERDEEN AB25  
22D//SCOTLAND/ (REPRINT); UNIV ABERDEEN, DEPT CELL & MOL BIOL/ABERDEEN  
AB25 22D//SCOTLAND/; UNIV MASSACHUSETTS, SCH MED, DEPT MOL PHARMACOL &  
TOXICOL/WORCESTER/MA/01555; DE MONTFORT UNIV, DEPT PHARMACEUT  
SCI/LEICESTER LE1 9BH/LEICS/ENGLAND/

JOURNAL: CANCER RESEARCH, 1997, V57, N14 (JUL 15), P3026-3031  
ISSN: 0008-5472 Publication date: 19970715

Publisher: AMER ASSOC CANCER RESEARCH, PUBLIC LEDGER BLDG, SUITE 816, 150  
S. INDEPENDENCE MALL W., PHILADELPHIA, PA 19106

Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

...Abstract: brain, and testis, There was no detectable immunostaining for  
CYP1B1 in normal tissues. These results provide the basis for the  
development of novel methods of \*cancer\* diagnosis\* based on the  
identification of CYP1B1 in tumor cells and the development of  
anticancer drugs that are selectively activated in tumors by CYP1B1.  
...Identifiers--METABOLIZING ENZYME-SYSTEMS; MICROSOMAL \*EPOXIDE\*  
\*HYDROLASE\*; AMINO-ACID SEQUENCE; ADRENAL CYTOCHROME-P450; NEOPLASTIC  
LESIONS; GENE SUBFAMILY; BREAST-CANCER; HUMAN KIDNEY; HUMAN LIVER; RAT  
CYP1B1

9/3,K/3 (Item 2 from file: 34)

DIALOG(R) File 34: SciSearch(R) cited Ref Sci  
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 File 444: New England Journal of Med. 1985-2001/Aug W1  
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 File 457: The Lancet 1986-2000/Oct W1  
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. Set      Items      Description
S1         0          CANCER? WITH (MARKER? OR DIAGNOS?)
S2        97610       CANCER? (W) (MARKER? OR DIAGNOS?)
S3        347300      NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4         890        CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5         0          (S2 OR S3 OR S4) AND REGUCALCIN
S6         2          (S2 OR S3 OR S4) AND (TSC(W)22)
S7         1          RD (unique items)
>>>KWIC option is not available in file(s): 41, 77, 399

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7/3,K/1 (item 1 from file: 155)  
DIALOG(R) File 155:MEDLINE(R)

10852046 20526087 PMID: 11072240  
**Novel association of a diverse range of genes with renal cell carcinoma**  
 as identified by differential display.

Rae FK; Stephenson SA; Nicol DL; Clements JA  
 Centre for Molecular Biotechnology, School of Life Sciences, Queensland  
 University of Technology, Brisbane, Australia.  
 International Journal of Cancer. Journal international du cancer (UNITED  
 STATES) Dec 1 2000, 88 (5) p726-32, ISSN 0020-7136 Journal code:  
 Languages: ENGLISH  
 Document type: Journal Article  
 Record type: Completed

... G-protein signalling (RGS-5), Notch-3, Na,K-ATPase alpha subunit, HLA  
 class II antigen, ETS-like protein, transforming growth factor  
 beta-stimulated clone (\*TSC\*22\*), bladder cancer-related protein (BC10)  
 and adipophilin. Semi-quantitative RT-PCR using specific primers to each of  
 these genes confirmed differential expression in 67% to...  
 ! Blotting, Northern; Carcinoma, Renal Cell--diagnosis--DI; DNA,  
 Complementary--analysis--AN; Kidney \*Neoplasms\*--\*diagnosis\*--DI; Reverse  
 Transcriptase Polymerase Chain Reaction  
 ?s (s2 or s3 or s4) and (epoxide(w)hydrolase)

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97610 S2
347300 S3
890 S4
94405 EPOXIDE
171611 HYDROLASE
13169 EPOXIDE(W)HYDROLASE
S8
18 (S2 OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)
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...completed examining records  
 S9 17 RP (unique items)  
 ?show files;ds;t/3,k/all

File 5: Biosis Previews(R) 1969-2001/Jul W5  
 (c) 2001 BIOSIS  
 File 6: NTIS 1964-2001/Aug W3  
 Compadstr 2000 NTIS, Intl Copyright All Right  
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 File 76: Life Sciences Collection 1982-2001/May



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... and 50/162 (31%) HIV-'s [OR 4.1, 95% CI 2.6-6.4] and by SB in 76/222 (34%) and 19/141 (\*14%) [\*3%\*.3\*1.8-6.1], respectively. Pap smear showed SIL in 53/316 (17%) of HIV+'s and 9/208 (4%) HIV-'s [4.5, 2...  
; Adolescence; Adult; Blotting, Southern; Cervical Intraepithelial Neoplasia\*--\*Diagnosis\*--DI; Cervical Intraepithelial Neoplasia--Virology --VI; CD4 Lymphocyte Count; DNA, Viral--Analysis--AN; Ethnic Groups; Middle Age; Polymerase Chain Reaction; Risk Factors; Vaginal Smears

15/3/K/25 (Item 1 from file: 159)

DIALOG(R) File 159: Cancerlit

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01481564 99195577 PMID: 10095843

**Endoscopic pateris of primary gastric MALT lymphoma.**

Aoun JP; Moukareb N; Khoury S

Division of Gastroenterology, Saint Georges Hospital, Beirut, Lebanon.  
J Med Liban; 46 (3) p131-5 1998 (LEBANON) May-Jun 1998, ISSN 0023-9852 Journal Code: J1Z

Languages: ENGLISH

Document Type: Journal Article

Record type: Completed

... treated for primary gastric MALT lymphomas, were reviewed. Four main patterns were recognized: 1/Large ulcerations (n = 6, 42.9%), 2/Polypoid lesion (n = 2, \*14%\*.3\*%), \*3\*/Gastritis with small ulcerations (n = 4, 28.5%), and 4/Atypical mucosal relief (AMR): erythema, nodularity, edematous or infiltrated folds (n = 2, 14.3%). In...  
Major Descriptors: Lymphoma, Mucosa-Associated Lymphoid Tissue--diagnosis --DI; \*Stomach \*Neoplasms\*--\*diagnosis\*--DI



sequences: Lys-Ala-Val-Thr-Glu...

... lines, human cancer tissue, human cancer cells in sputa, and IgM, but not with normal human cells. The MAbs can be used for human lung cancer \*diagnosis\* and in particular, for detection of the mRNA coding for the protein sequence. In a preferred embodiment, lymphocytes are isolated from healthy human peripheral blood...

DESCRIPTORS: \*14\*-3\*-3\* protein, phospholipase-A2 human monoclonal antibody prep., hybridoma construction, appl. lung cancer \*diagnosis\* mammalian animal cell culture tumor enzyme EC-3.1.1.4 (Vol.14, No.24)

15/3,K/23 (Item 1 from file: 149)

DIALOG(R) File 149: TGG Health&Wellness DB(SM)  
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01951833 SUPPLIER NUMBER: 67161662 (USE FORMAT 7 OR 9 FOR FULL TEXT)

**Proteomics: new perspectives, new biomedical opportunities. (Seminar)**

Banks, Rosamonde E; Dunn, Michael J; Hochstrasser, Denis F; Sanchez, Jean-Charles; Blackstock, Walter; Pappin, Barry J; Selby, Peter J  
The Lancet, 356, 9243, 1749  
Nov 18, 2000

PUBLICATION FORMAT: Magazine/Journal; Refereed ISSN: 0099-5355  
LANGUAGE: English RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE:

Professional

WORD COUNT: 7033 LINE COUNT: 00604

... discriminate between CJD and other types of dementia with a sensitivity of 88% and specificity of 99%. (29) Sequencing identified them as members of the \*14\*-3\*-3\* family. The value of \*14\*-3\*-3\* proteins as discriminatory markers for CJD in patients with dementia has since been confirmed in several studies, (30,31) although clinical use in CJD has... (25) Genetic markers, detected cytogenetically or by mutation detection, are also now entering clinical practice, 58 but some changes likely to be important in \*carcinogenesis\*, \*diagnosis\*, and prognosis, such as abnormal expression of proto-oncogenes, may not be associated with a detectable genetic lesion. For proteins implicated in cancer, the use... of patients with Creutzfeldt-Jakob disease. N Engl J Med 1986; 315: 279-83. (30) Zerr I, Bodemer M, Gellner O, et al. Detection of \*14\*-3\*-3\* protein in the cerebrospinal fluid supports the diagnosis of Creutzfeldt-Jakob disease. Ann Neurol 1998; 43: 32-40. (31) Beaudry P, Cohen P, Brandel JP, et al. \*14\*-3\*-3\* protein, neuron-specific enolase, and S-100 protein in cerebrospinal fluid of patients with Creutzfeldt-Jakob disease. Dementia Geriatr Cogn Dis 1999; 10: 40-46. MJ, et al. Characterization of endothelial antigens associated with transplant-associated coronary artery disease. J Heart Lung Transplant 1995; 14: S188-97. (58) Sell S. \*Cancer\* markers\* of the 1990s: comparison of the new generation of markers defined by monoclonal antibodies and oncogene probes to prototypic markers. Clin Lab Med 1990; 10...

15/3,K/24 (Item 1 from file: 157)

DIALOG(R) File 157: Aidsline(F)

(c) Format only 2000 The Dialog Corporation. All rts. reserv.

00176175 95920227

**Genital human papillomavirus (HPV) infection and squamous intraepithelial lesions (SIL) on pap smear in women at risk for HIV infection.**

Klein RS; Shah K; Cu-Uvin S; Schuman P; Solomon L; Warren D; Burk RD  
Montefiore Einstein, Bronx NY.  
Natl Conf Hum Retroviruses Relat Infect (2nd) (UNITED STATES) Jan

29-Feb 2 1995, p90,  
Languages: ENGLISH

Document Type: MEETING ABSTRACTS

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with the phosphorylation-specific interaction between them. The protein and substrate are incubated in...

... and the level of interaction is compared to that of non-mutants and the mutated partner is diagnosed. Measurement of protein binding at TCA1-mediated \*14\*-3\*-3\* recognition sites could be used to detect cancers. (75pp)  
DESCRIPTORS: recombinant twenty-five C-associated protein-kinase-1 prep., expression in host cell, antibody, appl. \*cancer\* \*diagnosis\* enzyme EC-2.7.1.37 protein sequence DNA sequence tumor (Vol.17, No.9)

15/3,K/21 (Item 4 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs  
(c) 2001 Derwent Publ Ltd. All rts. reserv.

0216582 DBA Accession No.: 97-11703 PATENT

**Anti-\*14\*-3\*-3\* protein mouse monoclonal antibody and a method for the inspection of human lung cancer - hybridoma cell culture**

CORPORATE SOURCE: Japan.

PATENT ASSIGNEE: Morinaga 1997

1997

PATENT NUMBER: JP 9187291 PATENT DATE: 970722 WPI ACCESSION NO.:

97-419404 (9739)

PRIORITY APPLIC. NO.: JP 9618031 APPLIC. DATE: 960109

NATIONAL APPLIC. NO.: JP 9618031 APPLIC. DATE: 960109

LANGUAGE: JA

**Anti-\*14\*-3\*-3\* protein mouse monoclonal antibody and a method for the inspection of human lung cancer**

ABSTRACT: A new mouse monoclonal antibody (MAb) recognizing \*14\*-3\*-3\* protein can be contained in a reagent for the diagnosis of human lung cancer. In an example, \*14\*-3\*-3\* protein family was purified from cattle brain and seven isoforms were separated by reverse phase HPLC. They were identified by the elution site and SDS...

...protein and fused with mouse myeloma cell line P3-X63-Ag8-UI (P3UI). The used cell (hybridoma) was cultured and screened for production of anti-\*14\*-3\*-3\* MAb by yeast-labeling immunoassay. The MAb was produced and purified. The reactivity of the MAb was tested by immunoblotting and checked by ELISA against each form of \*14\*-3\*-3\* protein. The reactivity against cancer tissue was also investigated.

DESCRIPTORS: cattle brain \*14\*-3\*-3\* protein tumor-associated antigen mouse monoclonal antibody, hybridoma, appl. human lung \*cancer\* \*diagnosis\* cell culture mammal animal (Vol.16, No.23)

15/3,K/22 (Item 5 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs  
(c) 2001 Derwent Publ Ltd. All rts. reserv.

0186928 DBA Accession No.: 95-14443 PATENT

**Antibody against human lung cancer cells used for screening of human lung cancer - human monoclonal antibody preparation by hybridoma construction for use in lung \*cancer\* \*diagnosis\***

PATENT ASSIGNEE: Morinaga; New-Technol.Japan 1995

PATENT NUMBER: JP 7206900 PATENT DATE: 950808 WPI ACCESSION NO.:

95-309100 (9540)

PRIORITY APPLIC. NO.: JP 9417475 APPLIC. DATE: 940704

NATIONAL APPLIC. NO.: JP 9417475 APPLIC. DATE: 940704

LANGUAGE: JA

**- human monoclonal antibody preparation by hybridoma construction for use in lung \*cancer\* \*diagnosis\***

ABSTRACT: An antibody (Ab) is claimed, which recognises a protein, particularly \*14\*-3\*-3\* protein or cytoplasmic phospholipase-A2 (EC-3.1.1.4), and has the following protein sequence and its modified

The first part of the paper discusses the importance of understanding the cultural context of the research. It highlights the need for researchers to be sensitive to the values and beliefs of the communities they are studying. This is particularly important in the field of health research, where cultural differences can significantly impact the effectiveness of interventions.

The second part of the paper presents a case study of a health intervention in a rural community. The study found that the intervention was more successful when it was tailored to the local culture and beliefs. This suggests that a one-size-fits-all approach is not always the best solution.

The third part of the paper discusses the challenges of conducting research in a culturally diverse environment. It emphasizes the need for researchers to have a deep understanding of the community they are studying and to be open to learning from their participants.

The fourth part of the paper concludes by highlighting the importance of ongoing communication and collaboration between researchers and the communities they are studying. This is essential for ensuring that the research is relevant and useful to the community.

15/3,K/19 (Item 2 from file: 357)  
DIALOG(R) File 357: Derwent Biotechnology Abs  
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0247764 DBA Accession No.: 2000-02254 PATENT

Use of \*14\*-3\*-3\* sigma polypeptides and nucleic acids for the diagnosis  
or treatment of cancer- recombinant protein production via  
vector-mediated gene transfer and expression in host cell for therapy

AUTHOR: Hermeking H; Gelstein B; Kinzler K W  
CORPORATE SOURCE: Baltimore, MD, USA.  
PATENT ASSIGNEE: Univ. John-Hopkins 1999

PATENT NUMBER: WO 9931240 PATENT DATE: 19990624 WPI ACCESSION NO.:

PRIORITY APPLIC. NO.: US 210748 APPLIC. DATE: 19981215

NATIONAL APPLIC. NO.: WO 99US26924 APPLIC. DATE: 19991218  
LANGUAGE: English

Use of \*14\*-3\*-3\* sigma polypeptides and nucleic acids for the diagnosis  
or treatment of cancer

ABSTRACT: The use of \*14\*-3\*-3\* sigma proteins and nucleic acids for  
developing agents for the diagnosis, determining susceptibility to or  
for treating cancers and identifying agents for treating cancers, is  
new. Also claimed are: a method for suppressing the growth of a tumor  
which involves administering a \*14\*-3\*-3\* sigma 248 amino acid  
protein sequence (II), which has a 1,320 bp DNA sequence (I) (both  
specified) to the cells; a method for diagnosing cancer which involves  
testing a tissue to determine in the tissue expresses less \*14\*-3\*-3\*  
sigma protein than normal tissue; a \*14\*-3\*-3\* sigma reporter  
construction containing a \*14\*-3\*-3\* sigma transcription regulatory  
region covalently linked in a cis configuration to a gene encoding an  
assayable product; an antisense \*14\*-3\*-3\* alpha construct; a method  
for promoting cell growth via administration of the antisense  
construct; a method for screening for potential antitumor agents; a  
vector containing...

DESCRPTORS: recombinant \*14\*-3\*-3\* sigma protein prep., vector-mediated  
gene transfer, expression in host cell, antisense molecule, appl.  
\*cancer\* diagnosis\*, therapy, gene therapy DNA sequence protein  
sequence tumor (Vol.19, No.5)

15/3,K/20 (Item 3 from file: 357)

DIALOG(R) File 357: Derwent Biotechnology Abs  
(c) 2001 Derwent Publ Ltd. All rts. reserv.

0222751 DBA Accession No.: 98-04348 PATENT

DNA encoding the twenty-five C-associated protein-kinase-1 (TcAK1) -  
recombinant protein expression in host cell, antibody production and  
application to \*cancer\* diagnosis\*

AUTHOR: Plimica-Worms H

CORPORATE SOURCE: St. Louis, MO, USA.

PATENT ASSIGNEE: Univ. Washington-St. Louis 1998

PATENT NUMBER: WO 9801756 PATENT DATE: 980115 WPI ACCESSION NO.:

98-101198 (9809)

PRIORITY APPLIC. NO.: US 677298 APPLIC. DATE: 960709

NATIONAL APPLIC. NO.: WO 97US11721 APPLIC. DATE: 970703

LANGUAGE: English

- recombinant protein expression in host cell, antibody production and  
application to \*cancer\* diagnosis\*

..ABSTRACT: TcAK1 produced. An antibody specifically reactive with a  
Tackl-kinase or an internal C-terminal peptide is claimed. A method is  
claimed for creating a \*14\*-3\*-3\* recognition motif within a TcAK1  
substrate by incubating the substrate in a recombinant transformed  
cell. A method is claimed of detecting a mutation in a \*14\*-3\*-3\*  
protein or a TcAK1 substrate where the mutation prevents or intereferes



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15/3,K/16 (Item 4 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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127133100 CA: 127(10)133100v PATENT

Anti-14-3-3 mouse monoclonal antibodies, diagnostic agents for human lung

cancer, and diagnostic method

INVENTOR(AUTHOR): Setoguchi, Hiroko; Kamel, Masanori; Kato, Masatoshi

LOCATION: Japan,

ASSIGNEE: Morinaga and Co., Ltd.; Research Development Corp. of Japan

19970722

APPLICATION: JP 9618031 (19960109)

PAGES: 6 pp. COMEN: JPKXXAF LANGUAGE: Japanese CLASS: C12P-021/08A;

G07K-016/18B; G07K-016/32B; C12N-015/02B; G01N-033/53B;

15/3,K/17 (Item 5 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(c) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

123225953 CA: 123(17)225953w PATENT

Antibody to phospholipase A for lung cancer diagnosis

INVENTOR(AUTHOR): Sato, Susumu; Kamel, Masanori; Hashizume, Shuichi;

Nomoto, Kikuo; Murakami, Hirohori

LOCATION: Japan,

ASSIGNEE: Morinaga & Co.; Shingijutsu Kaohatsu Jigyodan; Nomoto Kikuo;

Murakami Hirohori

PATENT: Japan Kokai Tokkyo Koho ; JP 95206900 A2 ; JP 07206900 DATE:

950808

APPLICATION: JP 94174775 (940704) \*JP 93304187 (931203)

PAGES: 10 pp. COMEN: JPKXXAF LANGUAGE: Japanese CLASS: C07K-016/30A;

A61K-039/395B; C12P-021/08B; G01N-033/53B; G01N-033/574B; G01N-033/577B;

C12N 015/02; C12P-021/08J; C12P-001/91J

15/3,K/18 (Item 1 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs

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0254020 DBA Accession No.: 2000-08510 PATENT

New complex of a NLK1 protein and its interacting protein useful for

treating cancer, hyperproliferative disorder, neurodegenerative

disorder, cardiomyopathies, virus infections and metabolic disorders-

recombinant protein and interacting protein complex production via

vector plasmid-mediated gene transfer and expression in host cell for

\*cancer\* diagnosis\* and therapy

AUTHOR: Nandabalan K; Schultz V P; Yang M

CORPORATE SOURCE: New Haven, CT, USA.

PATENT ASSIGNEE: Curagen 2000

PATENT NUMBER: WO 00020448 PATENT DATE: 20000413 WPI ACCESSION NO.:

2000-303742 (2026)

PRIORITY APPLIC. NO.: US 167206 APPLIC. DATE: 19981006

NATIONAL APPLIC. NO.: WO 99US23314 APPLIC. DATE: 19991006

LANGUAGE: English

- recombinant protein and interacting protein complex production via vector

plasmid-mediated gene transfer and expression in host cell for \*cancer\*

\*diagnosis\* and therapy

...ABSTRACT: (C1) of an NLK1 protein and an NLK1

protein-interacting protein (IP), where NLK1 protein-IP is selected

from TrkA, protein-phosphatase-1-alpha, \*14\*-3\*-3\*-alpha,

alpha-tropomyosin, vimentin, p0071, Inl-1, IP-1, -2, -3, -4 or -5, is

new. Also claimed are: a purified complex (C2) which is...

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US 08 889-447-2

[illegible]







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S2	4	RD unique items

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2/3,K/1 (Item 1 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

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138104843 CA: 138(8)104843m JOURNAL

Differential regulation of functional gene clusters in overt coronary artery disease in a transgenic atherosclerosis-hypertensive rat model

AUTHOR(S): Herrera, Victoria L. M.; Didishvili, Tamara; Lopez, Lyle V.; Ruiz-Opazo, Nelson

LOCATION: Unit of Molecular Genetics, Whitaker Cardiovascular Institute, Section of Molecular Medicine, Evans Department of Medicine, Boston

JOURNAL: Mol. Med. (Baltimore, MD, U. S.) (Molecular Medicine (Baltimore, MD, United States))

DATE: 2002 VOLUME: 8 NUMBER: 7 PAGES: 367-375

COMMENT: NUMBER3 ISSN: 1076-1551 LANGUAGE: English PUBLISHER: Johns

Hopkins University Press

2/3,K/2 (Item 2 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

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131238831 CA: 131(18)238831v PATENT

Protein and cDNA sequences encoding a human TSC-22 homolog

INVENTOR(AUTHOR): Hillman, Jennifer L.; Lal, Preethi; Shah, Furai

LOCATION: USA

ASSIGNEE: Inocyte Pharmaceuticals, Inc.

PATENT: United States; US 5958600 A DATE: 19990928

APPLICATION: US 5958337 (19970708)

PAGES: 25 pp. COMMENT: USXXAM LANGUAGE: English CLASS: 43506000;

C12:001/68A; C12F:021/02B; C12N:001/21B; C12N:154/12B

2/3,K/3 (Item 3 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

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126260113 CA: 126(20)260113f JOURNAL

Molecular cloning and characterization of a transcription factor for the

C-type natriuretic peptide gene promoter

AUTHOR(S): Ohta, Shigeki; Shimokake, Yoshiyuki; Nagata, Kiyoshi

LOCATION: Shionogi Research Laboratories, Shionogi & Co., Ltd., Osaka, Japan, 553

JOURNAL: Eur. J. Biochem. DATE: 1996 VOLUME: 242 NUMBER: 3 PAGES:

460-466 COMMENT: EUBOJ1 ISSN: 0014-2956 LANGUAGE: English PUBLISHER:

Springer

2/3,K/4 (Item 4 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

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120316986 CA: 120(25)316986p JOURNAL

Cloning of rat Sertoli cell follicle-stimulating hormone primary response complementary deoxyribonucleic acid: regulation of TSC-22 gene expression

AUTHOR(S): Hamill, Katherine G.; Hall, Susan H.

LOCATION: Dep. Pediatrics, Univ. North Carolina, Chapel Hill, NC, 27599,

USA

JOURNAL: Endocrinology DATE: 1994 VOLUME: 134 NUMBER: 3 PAGES:



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File 65-Inside Conferences 1993-2003/ Feb W3  
 (c) 2003 CAB International  
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 File 103-Energy Solved 1974-2003/Jan B3  
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 File 144-Biol. & Agric. Index 1982-2003/Jan  
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 File 155-MEDLINE 1966-2003/ Feb W3  
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 File 156-ToxFile 1964-2003/Nov W3  
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 File 163-CAB Health 1983-2003/Jan  
 (c) 2003 CAB International  
 File 170-EMBASE Alert 2003/ Feb W3  
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 File 305-Analytical Abstracts 1983-2003/Jan W4  
 (c) 2003 Royal Soc Chemistry  
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 File 370-Science 1996-2003/Jan W3  
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 File 881-Compendex 1983-2003/ Feb W3  
 (c) 2003 Elsevier Eng. Infor Inc  
 File 99-Wilson Appl. Sci & Tech Abs 1983-2003/Jan  
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 File 514-MILIS 1983-2003/ Dec  
 (c) 2003 Action Potential  
 File 149-766 HealthWelfare DB SM 1976-2003/ Feb W1  
 (c) 2003 The Gale Group  
 File 159-Cancer 1976-2003/Dec  
 (c) format only 2003 Dialing Corporation  
 File 164-Allied & Complementary Medicine 1984-2003/Jan  
 (c) 2003 BLNHS  
 File 442-AMA Journals 1982-2003/ May B1  
 (c) 2003 Amer Med Assn - PARS/DARS apply  
 File 444-New England Journal of Med. 1985-2003/ Feb W3  
 (c) 2003 Mass. Med Soc

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text suggests that organizations should implement robust systems to track every detail, from small expenses to major investments.

2. The second part of the document addresses the challenges of data management in a rapidly changing environment. It highlights the need for flexible and scalable solutions that can adapt to new technologies and evolving data requirements. The author argues that organizations must invest in training and infrastructure to ensure they can effectively handle large volumes of data while maintaining its integrity and security.

3. The third part of the document focuses on the role of leadership in driving organizational success. It stresses that leaders must be visionaries who can inspire and motivate their teams to achieve common goals. The text provides several examples of successful leaders and their strategies, emphasizing the importance of clear communication, strategic planning, and a strong sense of purpose.

4. The fourth part of the document discusses the importance of innovation and continuous improvement. It argues that organizations must constantly seek out new ways to optimize their processes and products to stay competitive in the market. The text encourages a culture of experimentation and learning from failure, suggesting that innovation is not just a one-time event but a ongoing process.

5. The fifth part of the document concludes by summarizing the key points discussed throughout the document. It reiterates the importance of record-keeping, data management, leadership, and innovation, and offers final thoughts on the future of the organization. The author expresses optimism about the potential for growth and success, provided that the organization remains committed to these core principles.

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**\*File 8: Alert feature enhanced for multiple files, duplicates**

removal, customized scheduling. See HELP ALERT.

File 99: Wilson Appl. Sci & Tech Abs 1983-2003/Jan

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File 135: NewsRx Weekly Reports 1985-2003/Feb W1

(c) 2003 NewsRx

**\*File 135: New newsletters are now added. See Help News135 for the**

complete list of newsletters

File 266: EMBRAP 2003/Dec

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File 313: Cheming & Biotech Abs 1970-2003/Dec

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File 357: Derwent Biotech Res 1962-2003/Feb W3

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**\*File 357: File is now current. See HELP NEWS 357.**

Alert feature enhanced for multiple files, etc. See HELP ALERT.

File 356: Current Biotech Abs 1983-2003/Dec

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File 35: Dissertation Abs Online 1961-2003-Jan

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File 48: SPORTDISCUS 1961-2003/Feb

File 91: MANTIS(TM) 1960-2003/Oct

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File 159: Cancerlit 1973-2003/Oct

(c) format only Good Biolog Corporation

**\*File 159: Updating for Cancerlit has stopped due to end of year**

processing.

File 164: Allied & Complementary Medicine 1984-2003/Jan

(c) 2003 BHASIS

File 44: AMA Journals 1962-2003/May B1

(c) 2003 Amer Med Assn - FARS/LARS apply

File 44: New England Journal of Med. 1985-2003/Feb W3

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File 467: EXAMED(EM) 2003/Dec

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**\*File 467: For information about updating status please see Help News467.**

Set Items Description

25 TS022 (S) W112

processing

Processed 10 of 39 files

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Completed processing all files

20 TS022

18910788 RATT

ST 4 TS022 (S) RATT

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Completed examining records

S2 4 RD (unique items)

250w files/35/4/3/K all

File 5: Biocis Reviews R 1969-2003/Feb W2

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File 6: NTIS 1964-2003/Feb W2

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File 34: Search(R) Cited Ref Sci 1990-2003/Feb W2

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File 40: Enright(R) 1975-2003/Jan

File 50: CAB Abstracts 1972-2003/Jan



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 File 34: Search(R) cited Ref Sci 1990-2003/ Feb W2  
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 File 44: Envtline(R) 1975-2003/ Jan  
 File 50: CAB Abstracts 1972-2003/ Jan  
 (c) 2003 CAB International  
 \*File 50: Truncating CC codes is recommended for full retrieval. See Help News50 for details.  
 File 55: Inside Conferences 1997-2003/ Feb W3  
 (c) 2003 BLDSG all rts, reserch  
 File 66: Envtline(R) 1972-2003/ Jan  
 (c) 2003 Internl Academy of Santa Barbara  
 File 71: ELSEVIER BIOBASE 1994-2003/ Feb W3  
 (c) 2003 Elsevier Science B.V.  
 File 72: EMBASE 1974-2003/ Feb W3  
 (c) 2003 Elsevier Science B.V.  
 \*File 73: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.  
 File 94: IJST-Epins 1985-2003/ Feb W3  
 (c) 2003 Japan Science and Tech Corp(JST)  
 \*File 94: UDS have been adjusted to reflect current months data. There is no data missing.  
 File 98: General Sci Abs/Pull-Text 1984-2003/ Jan  
 (c) 2003 The HW Wilson Co  
 File 100: Energy Scitoc 1974-2003/ Jan B2  
 (c) 2003 contains copyrighted material  
 \*File 103: For access restrictions see Help Restrict.  
 File 143: Biol & Agric Index 1983-2003/ Jan  
 (c) 2003 The HW Wilson Co  
 File 144: Biogest 1973-2003/ Feb W2  
 (c) 2003 INIST/CNRS  
 File 156: MEDLINE(R) 1964-2003/ Feb W2  
 (c) format only 2003 The Ltag Corp.  
 File 156: Toxline 1964-2003/ Nov W2  
 (c) format only 2003 The Ltag Corporation  
 \*File 156: TOXLINE Special data is now available. See Help News156.  
 File 162: CAB Health 1984-2003/ Jan  
 (c) 2003 CAB International  
 \*File 162: Truncating CC codes is recommended for full retrieval. See Help News162 for details.  
 File 172: EMBASE Alert 2002/ Feb W2  
 (c) 2003 Elsevier Science B.V.  
 File 305: Analytical Abstracts 1980-2003/ Jan W4  
 (c) 2003 Royal Soc Chemistry  
 \*File 305: Alert feature enhanced for multiple files, duplicate removal, customized scheduling. See HELP ALERT  
 File 366: New Scientist 1994-2003/ Feb W2  
 (c) 2003 Reed Business Information Ltd.  
 File 370: Science 1996-1999/ Jul W2  
 (c) 1999 WATS  
 \*File 370: This file is closed (no updates). Use File 47 for more current information.  
 File 399: CA SEARCH(R) 1967-2003/ CD=13808  
 (c) 2003 American Chemical Society  
 399: Use is subject to the terms of your user/customer agreement. Feature enhanced for multiple files, etc. See HELP ALERT.  
 134: Search(R) cited Ref Sci 1974-1989/ Dec  
 (c) 1988 Inst for Sci Info  
 98: Compendex(R) 1970-2003/ Feb W2













Country: us-09-490-609b-317.rge  
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Country	Match Length	DB	ID	Lower ID
1	259.2	91.9	1466	11	KA1522A	1.1765 KA1522A
2	175.4	62.2	1706	11	MB1522A	X.540 MB1522A
3	114.2	40.5	1718	78	HSB4604M	0.604H BHB4604M
4	114.2	40.5	1725	78	HS1522A	AL1522A BHB4604M
5	114.2	40.5	165164	66	AL169184	AL169184 BHB4604M
6	114.2	40.5	589575	67	AL169184	AL169184 BHB4604M
7	91.9	52.1	772	81	AB975662	AB975662 BHB4604M
8	90.4	52.1	435	48	1485885	AB975662 BHB4604M
9	69.8	24.8	1461	4	MB1522A	MB1522A BHB4604M
10	37.4	13.3	978	4	AP012462	AP012462 BHB4604M
11	36.3	12.9	554	11	MB1522A	MB1522A BHB4604M
12	36.3	12.9	623	65	AB975662	AB975662 BHB4604M
13	36.3	12.9	16929	59	AB975662	AB975662 BHB4604M
14	36.3	12.9	196057	59	AB975662	AB975662 BHB4604M
15	36.2	12.8	204318	11	AB975662	AB975662 BHB4604M
16	36	12.8	111222	6	AB975662	AB975662 BHB4604M
17	36	12.8	151948	59	AB975662	AB975662 BHB4604M
18	36	12.8	164528	8	AB975662	AB975662 BHB4604M
19	36	12.8	165507	58	AB975662	AB975662 BHB4604M
20	35.4	12.6	119947	8	AB975662	AB975662 BHB4604M
21	35	12.4	42501	32	AB975662	AB975662 BHB4604M

























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00M module: module search: using sw model

from 001: April 11, 2001, 13:09:04: Search Time: 044.44 Seconds  
(without all points)  
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2nd Pass: 2nd  
3rd Pass: 1st and 2nd of 1st pass only, 0.29, 500 Mbit/sec cell updates/sec

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5th Pass: 0.29, 500 Mbit/sec cell updates/sec

6th Pass: 7901 142 8000, 0003 74 0000 00000000

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8th Pass: Minimum for seq length: 10

9th Pass: Maximum for seq length: 20000000

10th Pass: First Processed: Minimum Match: 96  
Maximum Match: 1000  
Last and First 45 summaries

11th Pass: First:

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 COMMENT

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 The University of Oklahoma, 620 Parrington Hall, Room 208, Norman,  
 OK 73069, USA  
 on Sep 30, 2000 This sequence version replaced 9139954/67.  
 \* NOTE: This is a "working draft" sequence. It contains  
 \* statistics of 22 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
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 \* This record will be updated with the finished sequence  
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\*\*\*\*\*  
 1 2448: contig of 2448 bp in length  
 2449 2548: gap of unknown length  
 2549 5909: contig of 3460 bp in length  
 5909 91203: contig of 8112 bp in length  
 91203 92203: gap of unknown length  
 92203 13040: contig of 4720 bp in length  
 13040 19734: gap of unknown length  
 19734 19844: contig of 4694 bp in length  
 19844 22751: gap of unknown length  
 22751 22851: contig of 917 bp in length  
 22851 22852: gap of unknown length  
 22852 40058: contig of 7206 bp in length  
 40058 42704: gap of unknown length  
 42704 47204: contig of 7046 bp in length  
 47204 47205: gap of unknown length  
 47205 47206: contig of 7096 bp in length  
 47206 44401: gap of unknown length  
 44401 44402: gap of unknown length  
 44402 51430: contig of 6934 bp in length  
 51430 51431: gap of unknown length  
 51431 61086: contig of 9551 bp in length  
 61086 61087: gap of unknown length  
 61087 71097: contig of 9911 bp in length  
 71097 71098: gap of unknown length  
 71098 80500: contig of 9403 bp in length  
 80500 80501: gap of unknown length  
 80501 80502: contig of 8894 bp in length  
 80502 80503: gap of unknown length  
 80503 100616: contig of 11022 bp in length  
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 100716 111693: contig of 10673 bp in length  
 111693 111694: gap of unknown length  
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 121883 121884: gap of unknown length  
 121884 142844: contig of 19815 bp in length  
 142844 142944: gap of unknown length  
 142944 145198: contig of 12250 bp in length  
 145198 145208: gap of unknown length  
 145208 163223: contig of 17924 bp in length  
 163223 163224: gap of unknown length  
 163224 180088: contig of 17546 bp in length  
 180088 180089: gap of unknown length  
 180089 206059: contig of 27961 bp in length  
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 The University of Oklahoma

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 /Organization: "Mus musculus"  
 /DB Xref: "Taxon: 10090"  
 /Feature: "1P23: 41101"

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 145198 145208: gap of unknown length  
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 163223 163224: gap of unknown length  
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 180089 206059: contig of 27961 bp in length  
 206059 206060: gap of unknown length

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 The University of Oklahoma

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 /Organization: "Mus musculus"  
 /DB Xref: "Taxon: 10090"  
 /Feature: "1P23: 41101"

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[illegible]



Contract: Sequence Submissions 'openway.mt.mut.cedu'  
 Project Information  
 Contract project name: L11124  
 Contract name: 609 E.LB

NOTE: This record contains all individual sequencing reads that have not been assembled into contigs. Reads of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be over-represented. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 742: contig of 742 bp in length  
 743: gap of 100 bp in length  
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 1569 1568: gap of 100 bp in length  
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 2002 2491: gap of 100 bp in length  
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 4263 4262: gap of 100 bp in length  
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 9012 9111: gap of 100 bp in length  
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 12412 12411: gap of 100 bp in length  
 12413 13202: contig of 761 bp in length  
 13203 13892: gap of 100 bp in length  
 13893 14683: contig of 748 bp in length  
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 20763 21495: contig of 743 bp in length  
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 22309 22408: gap of 100 bp in length  
 22409 23100: contig of 746 bp in length  
 23101 23200: gap of 100 bp in length  
 23201 23975: contig of 689 bp in length

23976 24075: gap of 100 bp in length  
 24076 24814: contig of 749 bp in length  
 24815 24914: gap of 100 bp in length  
 24915 25600: contig of 746 bp in length  
 25601 25750: gap of 100 bp in length  
 25751 26477: contig of 727 bp in length  
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 28278 29019: contig of 742 bp in length  
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 31552 31651: gap of 100 bp in length  
 31652 32385: contig of 744 bp in length  
 32386 32485: gap of 100 bp in length  
 32486 33220: contig of 745 bp in length  
 33221 33320: gap of 100 bp in length  
 33321 34052: contig of 742 bp in length  
 34053 34152: gap of 100 bp in length  
 34153 34847: contig of 685 bp in length  
 34848 34947: gap of 100 bp in length  
 34949 35651: contig of 714 bp in length  
 35652 35751: gap of 100 bp in length  
 35752 36466: contig of 719 bp in length  
 36467 36566: gap of 100 bp in length  
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 38106 38205: gap of 100 bp in length  
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 38941 39040: gap of 100 bp in length  
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 41509 42250: contig of 742 bp in length  
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 43072 43171: gap of 100 bp in length  
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 48966 49675: contig of 720 bp in length  
 49676 49775: gap of 100 bp in length  
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C 23	31.2	19.8	14971	11	FNPSCA	Y13319 Homo sapi
C 24	31.2	18.8	172855	65	AC079446	AC079446 Homo sapi
C 25	31.2	18.8	190439	50	AC074741	AC074741 Homo sapi
C 25	31.1	18.6	206145	41	AC015236	A1193449 Homo sapi
C 26	31	18.7	3219	8	AC021834	AC021834 Homo sapi
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C 27	31	18.7	65955	65	AC069012	AC069012 Homo sapi
C 29	31	18.7	148219	38	AC066812	AC066812 Homo sapi
C 30	31	18.7	157717	38	AC010336	AC010336 Homo sapi
C 31	31	18.7	169489	30	AC010188	AC010188 Homo sapi
C 32	31	18.7	179865	57	AC068297	AC068297 Homo sapi
C 33	31	18.7	173787	55	AC046135	AC046135 Homo sapi
C 34	31	18.6	93349	37	AL132492	AL132492 Homo sapi
C 35	30.9	18.6	168516	84	HSS171M3	Contribution (4 of
C 36	30.8	18.6	155934	50	AC052449	AC052449 Homo sapi
C 37	30.9	18.6	155934	40	AC015914	AC015914 Homo sapi
C 38	30.8	18.6	169930	49	AC021541	AC021541 Homo sapi
C 39	30.8	18.6	188260	38	AC011368	AC011368 Homo sapi
C 40	30.8	18.6	201129	38	AC015610	AC015610 Homo sapi
C 41	30.8	18.6	206161	40	AC015915	AC015915 Homo sapi
C 42	30.8	18.6	209816	68	AL366130	AL366130 Homo sapi
C 43	30.8	18.6	210136	84	HES3110	AL133492 Homo sapi
C 44	30.6	18.6	340000	77	HS210162	AL163302 Homo sapi
C 45	30.6	18.4	184909	11	MM1223837	A1223837 Homo sapi

## ALIGNMENTS

AC013812	Homo sapi
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AF074747	Homo sapi
AF077741	Mus muscu
AF115186	Homo sapi
AF021404	Homo sapi
AF022426	Homo sapi
AF060812	Homo sapi
AC010336	Homo sapi
AC010188	Homo sapi
AC068629	Homo sapi
AC094135	Homo sapi
AF173102	Homo sapi
Continuation (4 of 4)	
AC022440	Homo sapi
AC015914	Homo sapi
AC012151	Homo sapi
AC011358	Homo sapi
AC015915	Mus muscu
AF135130	Homo sapi
AF133402	Homo sapi
AF163302	Homo sapi
AF125837	Mus muscu

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DEFINITION	D17447 3410 bp mRNA R0D 04-FEB-1999 Rattus norvegicus mRNA for 14-3-3 protein, gamma-subtype, complete cds.
ACCESSION	D17447
VERSION	D17447.1 GI:402525
KEYWORDS	14-3-3 protein, gamma-subtype, regulation of protein kinase C, Rattus norvegicus (strain:Wistar) postnatal day 21 brain cDNA, mRNA.
SOURCE	Rattus norvegicus
ORGANISM	Fukushima, Matsuda, Choudhry, Vellody, Mammalia, Eutheria, Rodentia, Scleroglossi, Muridae, Murinae, Rattus: 1 (bases 1 to 3410)
REFERENCE	Watanabe, M. Direct Submission Submitted (16 Aug 1993) to the EMBL/GenBank databases Masahito Watanabe, Hokkaido University School of Medicine, Department of Anatomy, Nishi-15 Kita-7, Kita-ku, Sapporo 060, Jpn (Tel:011-17-11330, Fax:011-717-5286) 2 (bases 1 to 3410)
REFERENCE	Watanabe, M., Isebe, T., Ichimura, T., Kuroda, R., Takahashi, Y. and Kuroda, H. Molecular cloning of rat cDNAs for beta and gamma subtypes of 14-3-3 protein and developmental changes in expression of their mRNAs in the nervous system Brain Res. Mol. Brain Res. 17 (1-2), 135-146 (1993)
JOURNAL	93164855
MEDLINE	3 (sites)
REFERENCE	Watanabe, M., Isebe, T., Ichimura, T., Kuroda, R., Takahashi, Y., Kondo, H. and Inoue, Y. Molecular cloning of rat cDNAs for the alpha and beta subtypes of 14-3-3 protein and differential distributions of their mRNAs in the brain Brain Res. Mol. Brain Res. 25 (1-2), 113-121 (1994)
JOURNAL	95075241
MEDLINE	
FEATURES	Location/Qualifiers 1..3410
SOURCE	

[illegible][illegible]

GenView Version 4.5  
Copyright (c) 1993-2000 CompuLink Ltd.

cm nucleotide nucleotide search, using sw model

Run on: April 11, 11, 2001, 18:02:55 Search time 4464.91 Seconds  
(601 hour alignments)  
190.272 Million cell updates/sec

Filter: 05:09 490 609b 488

Post filter score: 166

Scoring method: 1: reversed and reversed, ... approach of alignment 166

Scoring table: IDENTITY NUC  
Gapop: 10.0, Gapext: 1.0

Searches: 118433 Searches, 2558875100 residues

Total number of hits satisfying chosen parameters: 2286266

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database:

cmdb01:  
1: qb\_ba1:  
2: qb\_ba2:  
3: qb\_om:  
4: qb\_om:  
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Result No.	Score	* Match	Length	DB ID	Description
1	140	84.3	4410	11	017447
2	140	84.3	4410	11	S55405
3	85.2	51.3	198701	65	A0083753
4	84.4	20.7	164494	10	A0020898
5	84	20.5	672224	65	A0080050
6	84	20.5	69260	55	A0048377
7	84	20.5	191573	39	A0012486
8	82.8	19.8	180490	58	A0069152
9	82.5	19.6	97916	77	HS308822
10	82.6	19.6	206059	59	A0074312
11	82.6	19.5	226059	65	A0079488
12	82.6	19.6	243275	59	A0074705
13	82.4	19.5	52358	77	HS27610
14	82.4	19.5	171941	53	A0026531
15	82.4	19.5	175170	66	A0084815
16	82.2	19.4	166504	54	A0044779
17	82.2	19.4	181629	59	A0099978
18	82	19.3	190000	29	A0007108
19	81.8	19.2	203818	65	A0079644
20	81.4	19.0	178710	10	A0011477
21	81.4	18.9	166978	8	A0004098

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Thu Apr 12 10:22:21 2001

us-09-490-609b-318.rni

Page 8

















100

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Access DB# 39471

# SEARCH REQUEST FORM

Scientific and Technical Information Center

*[Signature]*

Requester's Full Name: \_\_\_\_\_  
Art Unit: \_\_\_\_\_  
Phone Number 30 \_\_\_\_\_  
Serial Number: \_\_\_\_\_  
Examiner #: \_\_\_\_\_  
Date: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_  
Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.  
\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or unity of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_  
Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_  
\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Vendors and cost where applicable

STAFF USE ONLY  
Searcher: *Edmond - July*  
Searcher Phone #: *308-4501*  
Searcher Location: *Booth 816*  
Date Searcher Picked Up: *4/9/01*  
Date Completed: *4/13/01*  
Searcher Prep & Review Time: *8 min*  
Online Time: *3 min*

Type of Search: *7*  
NA Sequence (#): \_\_\_\_\_  
AA Sequence (#): \_\_\_\_\_  
Structure (#): \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Fulltext: \_\_\_\_\_  
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Questel/Orbit: \_\_\_\_\_  
Dr Link: \_\_\_\_\_  
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Sequence Systems: *AB5501*  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

PTO-1590 (1-2000)



STIC-Biotech/ChemLib

39491

CRFG

From:

Sent:

To:

Subject:

Lacourciere, Karen  
Friday, April 06, 2001 3:37 PM  
STIC-Biotech/ChemLib  
Sequence Search 09/490,609

Please search the following sequences for 09/490609 in both the commercial databases and the inference database:

SEQ ID NO: 317, 318, 280, 337, 465, 488, and 384.

Thank-you!

*Karen A. Lacourciere Ph.D.*  
CM1 11D09 GAU 1635  
(703) 308-7523





The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus
<220> FEATURE:
<223> OTHER INFORMATION: unsure at all n locations
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OTHER INFORMATION: unsure at all in locations  
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164



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same {

same {

44

09/490,604



} Same

} Same

} Same

p 3

09/490,609



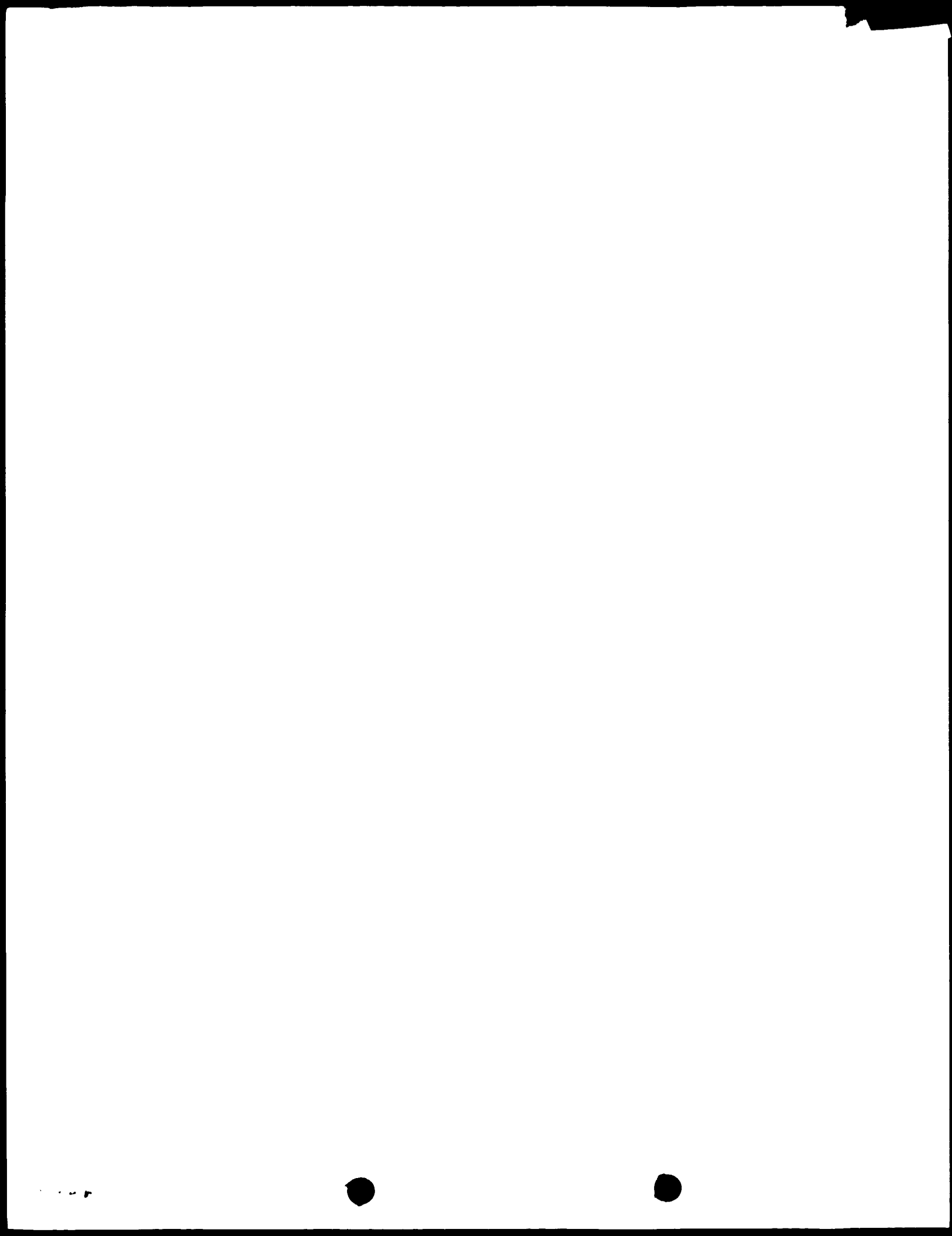
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USPT.PGPB.JPAB.EPAB.DWPI.TDBD	(11 or 12 or 13 or 14 or 15 or 16) and annexin with II	5	L11
USPT.PGPB.JPAB.EPAB.DWPI.TDBD	(11 or 12 or 13 or 14 or 15 or 16) and annexin	93	L10
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(c) Format only 2000 The Dialog Corporation  
 File 157: Aidsline(R) 1980-2000/Dec  
 (c) Format only 2000 The Dialog Corporation  
 File 159: Cancerlit 1975-2001/Jun  
 (c) Format only 2001 Dialog Corporation  
 File 164: Allied & Complementary Medicine 1984-2001/Aug  
 (c) 2001 BLHCIS  
 File 442: AMA Journals 1982-2001/Jul B3  
 (c) 2001 Amer Med Assn - FARS/LARS apply  
 File 444: New England Journal of Med. 1985-2001/Aug W1  
 (c) 2001 Mass. Med. Soc.  
 File 457: The Lancet 1986-2000/Oct W1  
 (c) 2000 The Lancet, Ltd.  
 File 467: Extramed(tm) 2000/Dec  
 (c) 2001 Informantia Ltd.

Set	Items	Description
S1	0	CANCER? WITH (MARKER? OF DIAGNOS?)
S2	97610	CANCER? (W) (MARKER? OF DIAGNOS?)
S3	347300	NEOPLAS? (W) (MARKER? OF DIAGNOS?)
S4	890	CARCINOGEN? (W) (MARKER? OF DIAGNOS?)
S5	0	(S2 OF S3 OF S4) AND REGUCALCIN
S6	0	(S2 OF S3 OF S4) AND (TSC(W)22)
S7	1	RD (unique items)
S8	18	(S2 OF S3 OF S4) AND (EPOXIDE(W)HYDROLASE)
S9	17	RD (unique items)
S10	5	(S2 OF S3 OF S4) AND BTF
S11	0	RD (unique items)
S12	0	(S2 OF S3 OF S4) AND (ANNEXIN(W)II)
S13	0	RD (unique items)
S14	40	(S2 OF S3 OF S4) AND (14(W)3(W)3)
S15	20	RD (unique items)



File 34:SciSearch(R) Cited Ref Set 1990-2001/Aug WI  
 (c) 2001 Inst for Sci Info  
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 (c) 2001 Congressional Information Service  
 41:Publication Abs 1970-2001 Aug  
 (c) 2001 Cambridge Scientific Abstracts  
 50:CAB Abstracts 1975-2001 Jul  
 (c) 2001 CAB International  
 65:Inside Conferences 1993-2001/Aug WI  
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 66:Environline 1974-2001 Jul  
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 71:ELISEVIER BIOBASE 1994-2001/Aug WI  
 (c) 2001 Elsevier Science B.V.  
 73:EMBASE 1974-2001 Jul M5  
 (c) 2001 Elsevier Science B.V.  
 76:Life Sciences Collection 1987-2001/May  
 (c) 2001 Cambridge Sci Abs  
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 94:ICIST-EPIS 1991-2001/Jul M5  
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 File 156:TOXLINE(F) 1963-2000/Dec  
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 File 172:EMBASE Alert 2001/Aug WI  
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 File 364:New Scientist 1994-2001 Jul M3  
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 (c) 2001 WVA  
 File 390:SciSearch(F) 1967-2001/Dec M5  
 (c) 2001 AMERICAN CHEMICAL SOCIETY  
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 File 161:Healthstar 1973-2000/Dec

Thu Apr 12 10:22:41 2001

us-09-490-609b-488.rst

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Page 10









Matches 48: Conservative 44 Mismatches 50 Indels 0 Gaps 0

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Best Local Similarity 26.9% Prod No 9.6;  
Matches 36; Conservative 48; Mismatches 50; Indels 0; Gaps 0;

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QY 89 [\[...\]](#) 14.9

DB 1014 [\[...\]](#) 14.9

QY 149 [\[...\]](#) 14.9

DB 953 [\[...\]](#) 14.9

RESULT 9

FEATURES

source

location/qualifiers

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/clone="11b"

/clone="BACN03812"

/note="end : Stop"

BASE COUNT

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ORIGIN

Submitted (24 Jun 1999) Genoscope - Centre National de Séquençage  
BP 191 91006 Evry Corbeil FRANCE (E-mail : seq@genoscope.cns.fr  
Web : www.genoscope.cns.fr)  
determination of this BAC end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
[http://www.edgp.org.uk](#) . This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billard at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MPG  
project grant . The DNA was prepared from embryos by Alain Billard  
and Genevieve Payan . It has been constructed in the vector  
pBacN03812 .

Accession

Version

Keywords

Source

Organism

Plasmid Drosophila melanogaster

Barry J. McQuinn, Artthropod Fracture, Hexapoda, Insecta;  
Phylogeny, Neoptera, Euphydryinae, Diptera, Ephydra;  
Muscularia, Phlebotoma, Drosophilidae, Drosophila.

REFERENCE

1 (bases 1 to 1101)

AUTHORS

TITLE

Journal

Submitted (24 Jun 1999) Genoscope - Centre National de Séquençage  
BP 191 91006 Evry Corbeil FRANCE (E-mail : seq@genoscope.cns.fr  
Web : www.genoscope.cns.fr)  
determination of this BAC end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
[http://www.edgp.org.uk](#) . This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billard at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MPG  
project grant . The DNA was prepared from embryos by Alain Billard  
and Genevieve Payan . It has been constructed in the vector  
pBacN03812 .

AW61421/c

LOCUS

AW61421 340 bp mRNA

DEFINITION

AW61421 171199-231-334-33524 Homo sapiens cDNA, mRNA sequence

ACCESSION

AW61421

VERSION

AW61421.1 GI:6666071

KEYWORDS

EST

SOURCE

human

ORGANISM

Homo sapiens

Cell type: M4209; Character: General; Worktype: Post-postnatal;  
Mammalian; Further: Human; Catalog: Catalog; Identifier: Homo.

REFERENCE

1 (bases 1 to 340)

HPG [http://www.hgi.org/](#) HGP ESTS

THE PATENT/EST Human Cancer Genome Project

UNPUBLISHED (1999)

CONTACT: Simpson A.J.G.

LABORATORY OF Cancer Genetics

INDIA Institute for Cancer Research

INDIA Prot. Antonio Prudente 109, 4 andar, 0509-010, Sao Paulo-SP,  
Brazil

TEL: +55-11-2704922

FAX: +55-11-2707001

EMAIL: [asimpson@india.org.br](#)

THIS sequence was derived from the PATENT/EST Human Cancer Genome  
Project. This entry can be seen in the following DBL

DATE: 2000-1-14; 14:15:11; 2/2/2000; 1/2/2000; 2/2/2000; 2/2/2000;  
1/1/2000-01-04; 04/04/1999 11:15:14-1)

Seq primer: puc 16 forward

High quality sequence start: 7

High quality sequence stop: 277

location/qualifiers

1. 340

/organism="Homo sapiens"

/clone="11b"

/clone="11b"

/clone="11b"

/note="end : Stop"

BASE COUNT

100 a 106 c 56 g 78 t

ORIGIN

Query Match

19.8% Score 32.81 DH 89; Length 140;  
Best Local Similarity 26.9% Prod No 9.1;  
Matches 65; Conservative 49; Mismatches 56; Indels 0; Gaps 0;

DB 258 [\[...\]](#) 10.14

QY 105 [\[...\]](#) 14.9

DB 139 [\[...\]](#) 14.9

QY 165 [\[...\]](#) 14.9

DB 148 [\[...\]](#) 14.9

RESULT 10

AW61421/c

LOCUS

AW61421 340 bp mRNA

DEFINITION

AW61421 171199-231-334-33524 Homo sapiens cDNA, mRNA sequence

ACCESSION

AW61421

VERSION

AW61421.1 GI:6666071

KEYWORDS

EST

SOURCE

human

ORGANISM

Homo sapiens

Cell type: M4209; Character: General; Worktype: Post-postnatal;  
Mammalian; Further: Human; Catalog: Catalog; Identifier: Homo.

REFERENCE

1 (bases 1 to 340)

HPG [http://www.hgi.org/](#) HGP ESTS

THE PATENT/EST Human Cancer Genome Project

UNPUBLISHED (1999)

CONTACT: Simpson A.J.G.

LABORATORY OF Cancer Genetics

INDIA Institute for Cancer Research

INDIA Prot. Antonio Prudente 109, 4 andar, 0509-010, Sao Paulo-SP,  
Brazil

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FAX: +55-11-2707001

EMAIL: [asimpson@india.org.br](#)

THIS sequence was derived from the PATENT/EST Human Cancer Genome  
Project. This entry can be seen in the following DBL

DATE: 2000-1-14; 14:15:11; 2/2/2000; 1/2/2000; 2/2/2000; 2/2/2000;  
1/1/2000-01-04; 04/04/1999 11:15:14-1)

Seq primer: puc 16 forward

High quality sequence start: 7

High quality sequence stop: 277

location/qualifiers

1. 340

/organism="Homo sapiens"

/clone="11b"

/clone="11b"

/clone="11b"

/note="end : Stop"

BASE COUNT

100 a 106 c 56 g 78 t

ORIGIN







117: em\_estp16:\*

118: em\_estp17:\*

119: em\_estp18:\*

120: em\_estp14:\*

121: em\_estp15:\*

122: em\_estp16:\*

123: em\_estp17:\*

124: em\_estp18:\*

125: em\_estp19:\*

126: qb\_est58:\*

127: qb\_est59:\*

128: qb\_est60:\*

129: qb\_est61:\*

130: qb\_est62:\*

131: qb\_est63:\*

132: qb\_est64:\*

133: qb\_est65:\*

134: qb\_est66:\*

135: qb\_est75:\*

136: qb\_est76:\*

137: qb\_est77:\*

138: qb\_est78:\*

139: qb\_est79:\*

140: qb\_est80:\*

141: qb\_est81:\*

142: qb\_est82:\*

143: qb\_est83:\*

144: qb\_est84:\*

145: qb\_est85:\*

146: qb\_est86:\*

147: qb\_est87:\*

148: qb\_est88:\*

149: qb\_est89:\*

150: qb\_est90:\*

151: qb\_est91:\*

152: em\_qss21:\*

153: em\_qss22:\*

154: em\_qss23:\*

155: em\_qss24:\*

156: em\_qss25:\*

157: qb\_qss26:\*

158: qb\_qss27:\*

159: qb\_qss28:\*

160: qb\_qss29:\*

161: em\_qss30:\*

162: em\_qss31:\*

163: em\_qss32:\*

164: em\_qss33:\*

165: em\_qss34:\*

166: em\_qss35:\*

167: em\_qss36:\*

168: qb\_qss37:\*

169: qb\_qss38:\*

170: em\_qss39:\*

171: qb\_qss40:\*

172: qb\_qss41:\*

173: qb\_qss42:\*

174: qb\_qss43:\*

175: qb\_qss44:\*

176: qb\_qss45:\*

177: qb\_qss46:\*

178: qb\_qss47:\*

179: em\_qss48:\*

180: em\_qss49:\*

181: qb\_qss50:\*

182: qb\_qss51:\*

183: qb\_qss52:\*

184: qb\_qss53:\*

185: qb\_qss54:\*

186: em\_qss55:\*

187: em\_qss56:\*

188: em\_qss57:\*

189: em\_qss58:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83.6	50.4	497	AW047721	AW047721 01-M-BH1-A1592463 7111027
2	81.2	50.1	466	A1592463	A1592463 7111027
3	82	49.4	577	HE372124	HE372124 601227812
4	80.2	48.8	271	AU014748	AU014748 AU014748
5	71	42.8	293	AA720737	AA720737 7111027
6	68.8	23.4	1055	CNS00030	A1069499 10584911
7	63.6	20.2	1013	CNS01683	A1106871 10584911
8	62.6	19.8	1101	CNS06770	A1094287 10584911
9	62.6	19.6	449	AW261421	AW261421 601227812
10	62.2	19.4	529	AG237295	AG237295 HE372124
11	62	19.4	518	AM152647	AM152647 601227812
12	62	19.4	560	AM152701	AM152701 601227812
13	61.6	19.0	1093	CNS05003	A131819 10584911
14	61.6	19.0	1095	CNS05003	A131819 10584911
15	61.2	18.9	748	CNS04630	A1244287 10584911
16	61.2	18.8	742	AU0048537	AU0048537 601227812
17	61.2	18.8	888	CNS00000	A1072496 10584911
18	61.2	18.8	949	CNS04410	A1274929 10584911
19	61	18.7	298	W23904	W23904 601227812
20	61	18.7	406	AW250701	AW250701 601227812
21	61	18.7	558	AA292187	AA292187 601227812
22	61.1	18.7	611	AW047750	AW047750 115001021
23	61	18.7	638	AW059440	AW059440 115001021
24	61	18.7	651	AW752866	AW752866 115001021
25	61	18.7	727	AV189403	AV189403 115001021
26	61	18.7	1194	HE045576	HE045576 601227812
27	60.8	18.6	507	HE045576	HE045576 601227812
28	60.8	18.6	546	AW555535	AW555535 115001021
29	60.8	18.6	556	HE370972	HE370972 601227812
30	60.8	18.6	893	HE370972	HE370972 601227812
31	60.8	18.6	922	CNS00740	A1066784 10584911
32	60.8	18.6	991	CNS03400	A1293742 10584911
33	60.6	18.4	425	HE371999	HE371999 601227812
34	60.6	18.4	442	A1010612	A1010612 601227812
35	60.6	18.4	466	HE372124	HE372124 601227812
36	60.6	18.4	469	CNS04080	A1302290 10584911
37	60.6	18.4	480	HE104725	HE104725 01-R-BX0-
38	60.6	18.4	569	A1176084	A1176084 601227812
39	60.6	18.4	586	AW375005	AW375005 601227812
40	60.6	18.4	741	AW160065	AW160065 601227812
41	60.6	18.4	755	HE372124	HE372124 601227812
42	60.6	18.4	1047	HE372124	HE372124 601227812
43	60.4	18.3	308	AA657476	AA657476 601227812
44	60.4	18.3	430	AA292989	AA292989 601227812
45	60.3	18.3	576	AA509392	AA509392 10584911

## ALIGNED

RESULT 1

AW047721 397 bp mRNA EST 18-SEP-1999

LOCUS 01-M-BH1-A1592463 7111027 NIB-BH1-M-52 10584911

ACCESSION AW047721

VERSION AW047721.1

KEYWORDS EST

SOURCE mouse

CanPro version 4.5  
Copyright (c) 1993-2000 CanProton Ltd.

Can nucleon nucleon search, using sw model

Run on: April 11, 2001, 15:01:40 : Search Time: 644.34 Seconds

(with all arguments)  
447.824 Million cpi-1 updates/sec

Full set: DB: 09 490 609b 488

Database: 1 CanProtonCanProCanPro.....CanProCanProCanPro 166

Scoring table: IDENTITY.MTC

Gap: 10.0 : Gap: 1.0

Search: 7991742 seqs, 6503748708 residues

Total number of hits satisfying chosen parameters: 1598484

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match: 0%

Using first 45 summations

Database :

```

1:  db_0811: *
2:  db_0812: *
3:  db_0813: *
4:  db_0814: *
5:  db_0815: *
6:  db_0816: *
7:  db_0817: *
8:  db_0818: *
9:  db_0819: *
10: db_08110: *
11: db_08111: *
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13: db_08113: *
14: db_08114: *
15: db_08115: *
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111: db_08211: *
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113: db_08213: *
114: db_08214: *
115: db_08215: *
116: db_08216: *

```

```

44: db_08144: *
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46: db_08146: *
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49: db_08149: *
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111: db_08211: *
112: db_08212: *
113: db_08213: *
114: db_08214: *
115: db_08215: *
116: db_08216: *

```

190: qb\_gss25: \*  
191: qb\_gss26: \*  
192: qb\_gss27: \*  
193: qb\_gss28: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
C 1	184	63.7	448	17	A1170562	A1170562 EST216494
C 2	184	63.7	479	12	AA851056	AA851056 EST193824
C 3	184	63.7	480	24	A1713203	A1713203 UI-R-Y0-a
C 4	178.2	61.7	481	13	AA914539	AA914539 v202b02.r
C 5	172.8	59.8	502	4	AA268983	AA268983 v399307.r
C 6	172.8	59.8	656	18	A1256412	A1256412 ui84107.r
C 7	172.8	59.8	683	26	A1875662	A1875662 uk51b08.x
C 8	172.8	59.8	692	26	A1875662	A1875662 uk51b08.x
C 9	172.8	59.8	709	138	BF980156	BF980156 UI-M-B02-
C 10	172.8	59.8	721	16	A1118166	A1118166 ue38f05.x
C 11	172.8	59.8	744	23	A1647488	A1647488 uk42a09.x
C 12	172.8	59.8	829	17	A1195553	A1195553 ui52a11.x
C 13	171.2	59.2	411	4	AA238092	AA238092 mx78e05.r
C 14	171.2	59.2	484	104	BE133018	BE133018 ui34a01.x
C 15	171.2	59.2	561	25	A1786994	A1786994 uj51h05.x
C 16	170.8	59.1	496	104	BE133649	BE133649 uq04a09.x
C 17	169.8	58.8	793	16	A1114891	A1114891 ui49f06.x
C 18	169.8	58.8	829	17	A1236567	A1236567 EST233129
C 19	167	57.8	411	94	AW741912	AW741912 u997e03.y
C 20	167	57.8	523	7	AA422350	AA422350 v145d08.r
C 21	166.4	57.6	629	94	AW701821	AW701821 uq15a05.x
C 22	166.4	57.6	629	94	AW701821	AW701821 uq15a05.x
C 23	164.8	57.0	503	16	A1159703	BE133073 ui34h08.x
C 24	164.8	57.0	503	16	A1159703	BE133073 ui34h08.x
C 25	164.8	57.0	543	17	A1194773	A1159703 ui03d11.x
C 26	163.2	56.5	487	104	BE132873	A1194773 ui56e05.x
C 27	162.2	56.1	208	15	A1035435	BE132873 ui34d01.x
C 28	161.6	55.9	592	18	A1303360	A1035435 ub46e11.r
C 29	156.8	54.3	390	108	BE449103	A1303360 ui77d08.x
C 30	150.2	52.0	401	29	AW042738	BE449103 ui52a02.y
C 31	150	51.9	258	146	W18222	AW042738 AU042738
C 32	149.8	51.8	510	111	BE649120	W18222 m369h04.r
C 33	139.6	48.3	390	22	A1575136	BE649120 UI-M-BH1-
C 34	135.2	46.9	383	13	AA900551	A1575136 UI-R-E0-C
C 35	134.8	46.6	394	108	BE447635	AA900551 UI-R-E0-C
C 36	134.4	46.5	379	4	AA250517	BE447635 ui52e02.x
C 37	131.6	45.5	392	17	A1181916	AA250517 mw99a03.r
C 38	131.6	45.5	394	39	AW047588	A1181916 ud77a02.x
C 39	127	43.9	624	97	AW964180	AW047588 UI-M-BH1-
C 40	127	43.9	658	38	AW701709	AW964180 EST376253
C 41	127	43.9	683	38	AW703975	AW701709 AV701709
C 42	125.4	43.4	420	24	A1751826	AW703975 AV703975
C 43	125.4	43.4	473	8	AA487871	A1751826 cn12b03.x
C 44	125	43.3	571	105	BE236194	A1751826 cn12b03.x
C 45	121.8	42.1	412	23	A1676208	AA487871 ab13b07.s
						BE236194 143894 MA
						A1676208 wc72c09.x

## ALIGNMENTS

RESULT	1	A1170562	448 bp	mRNA	EST	20-JAN-1999
LOCUS	EST216494	Normalized rat lung			Rattus sp.	cDNA clone
DEFINITION	RLJQ081.3'	end, mRNA sequence.				
ACCESSION	A1170562					
VERSION	EST.					
KEYWORDS	Rattus sp.					
SOURCE						

```

GenCore version 4.5
Copyright (c) 1994 - 2000 CompuGen Ltd.

cm nucleic nucleic search, using sw model
Run on: April 11, 2001, 15:40:40 ; Search time 344.44 Seconds
        (without alignments)
        605,550 Million cell updates/sec

Title: US-09-490-609b-337
Percent Score: 289
Sequence: 1 atgaattcttatgcccac.....nngaaaaanttttccccc 289

Scoring Table: IDENTITY_NP
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503744858 residues 15986484
Total number of hits satisfying chosen parameters:

Minimum 18 seq length: 0
Maximum 18 seq length: 2000000000

Post processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database:
1: qb_est1 : *
2: qb_est2 : *
3: qb_est3 : *
4: qb_est4 : *
5: qb_est5 : *
6: qb_est6 : *
7: qb_est7 : *
8: qb_est8 : *
9: qb_est9 : *
10: qb_est10 : *
11: qb_est11 : *
12: qb_est12 : *
13: qb_est13 : *
14: qb_est14 : *
15: qb_est15 : *
16: qb_est16 : *
17: qb_est17 : *
18: qb_est18 : *
19: qb_est19 : *
20: qb_est20 : *
21: qb_est21 : *
22: qb_est22 : *
23: qb_est23 : *
24: qb_est24 : *
25: qb_est25 : *
26: qb_est26 : *
27: qb_est27 : *
28: qb_est28 : *
29: qb_est29 : *
30: qb_est30 : *
31: qb_est31 : *
32: qb_est32 : *
33: qb_est33 : *
34: qb_est34 : *
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36: qb_est36 : *
37: qb_est37 : *
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43: qb_est43 : *
44: qb_est44 : *
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49: qb_est49 : *
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56: qb_est56 : *
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59: qb_est59 : *
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64: qb_est64 : *
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66: qb_est66 : *
67: qb_est67 : *
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110: qb_est110 : *
111: qb_est111 : *
112: qb_est112 : *
113: qb_est113 : *
114: qb_est114 : *
115: qb_est115 : *
116: qb_est116 : *

```